



#5

SEQUENCE LISTING

<110> AGY Therapeutics
Melcher, Thorsten
Mueller, Sabine
Chin, Daniel

<120> USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZATION
OF BRAIN TUMORS

<130> 263/180 -- PEagleman -- AGY

<140> 09/983,000

<141> 2001-10-17

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<170> PatentIn version 3.1

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tac aga caa cag aga aaa ctt gtt gaa gag att ggc tgg tcc tat aca 270
Tyr Arg Gln Gln Arg Lys Leu Val Glu Glu Ile Gly Trp Ser Tyr Thr
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gga gca ctg aat caa aaa aat tgg gga aag aaa tat cca aca tgt aat 318
Gly Ala Leu Asn Gln Lys Asn Trp Gly Lys Lys Tyr Pro Thr Cys Asn
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agc cca aaa caa tct cct atc aat att gat gaa gat ctt aca caa gta 366
Ser Pro Lys Gln Ser Pro Ile Asn Ile Asp Glu Asp Leu Thr Gln Val
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aat gtg aat ctt aag aaa ctt aaa ttt cag ggt tgg gat aaa aca tca 414
Asn Val Asn Leu Lys Lys Leu Lys Phe Gln Gly Trp Asp Lys Thr Ser
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ttg gaa aac aca ttc att cat aac act ggg aaa aca gtg gaa att aat 462
Leu Glu Asn Thr Phe Ile His Asn Thr Gly Lys Thr Val Glu Ile Asn
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ctc act aat gac tac cgt gtc agc gga gga gtt tca gaa atg gtg ttt 510
Leu Thr Asn Asp Tyr Arg Val Ser Gly Gly Val Ser Glu Met Val Phe
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Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
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35 40 45

Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile
50 55 60

Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Lys Leu
65 70 75 80

Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
85 90 95

Asn Thr Gly Lys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
100 105 110

Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
115 120 125

His Trp Gly Lys Cys Asn Met Ser Ser Asp Gly Ser Glu His Ser Leu
130 135 140

Glu Gly Gln Lys Phe Pro Leu Glu Met Gln Ile Tyr Cys Phe Asp Ala
145 150 155 160

Asp Arg Phe Ser Ser Phe Glu Glu Ala Val Lys Gly Lys Gly Lys Leu
165 170 175

Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
180 185 190

Gln Ala Ala Leu Asp Pro Phe Ile Leu Leu Asn Leu Leu Pro Asn Ser
210 215 220

Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly Ser Leu Thr Ser Pro Pro Cys
225 230 235 240

Thr Asp Thr Val Asp Trp Ile Val Phe Lys Asp Thr Val Ser Ile Ser
245 250 255

Glu Ser Gln Leu Ala Val Phe Cys Glu Val Leu Thr Met Gln Gln Ser
260 265 270

Gly Tyr Val Met Leu Met Asp Tyr Leu Gln Asn Asn Phe Arg Glu Gln
275 280 285

Gln Tyr Lys Phe Ser Arg Gln Val Phe Ser Ser Tyr Thr Gly Lys Glu
290 295 300

Glu Ile His Glu Ala Val Cys Ser Ser Glu Pro Glu Asn Val Gln Ala
305 310 315 320

Asp Pro Glu Asn Tyr Thr Ser Leu Leu Val Thr Trp Glu Arg Pro Arg
325 330 335

Val Val Tyr Asp Thr Met Ile Glu Lys Phe Ala Val Leu Tyr Gln Gln
340 345 350

Leu Asp Gly Glu Asp Gln Thr Lys His Glu Phe Leu Thr Asp Gly Tyr
355 360 365

Gln Asp Leu Gly Ala Ile Leu Asn Asn Leu Leu Pro Asn Met Ser Tyr
370 375 380

Val Leu Gln Ile Val Ala Ile Cys Thr Asn Gly Leu Tyr Gly Lys Tyr
385 390 395 400

Ser Asp Gln Leu Ile Val Asp Met Pro Thr Asp Asn Pro Glu Leu Asp
405 410 415

Leu Tyr Tyr Asp Ile Val His Tyr Ala Ile Val Asn Ile Gly Asp Asp

435

440

445

Ser Ala Thr Asn Gln Ile Arg Lys Lys Glu Pro Gln Ile Ser Thr Thr
450 455 460

Thr His Tyr Asn Arg Ile Gly Thr Lys Tyr Asn Glu Ala Lys Thr Asn
465 470 475 480

Arg Ser Pro Thr Arg Gly Ser Glu Phe Ser Gly Lys Gly Asp Val Pro
485 490 495

Asn Thr Ser Leu Asn Ser Thr Ser Gln Pro Val Thr Lys Leu Ala Thr
500 505 510

Glu Lys Asp Ile Ser Leu Thr Ser Gln Thr Val Thr Glu Leu Pro Pro
515 520 525

His Thr Val Glu Gly Thr Ser Ala Ser Leu Asn Asp Gly Ser Lys Thr
530 535 540

Val Leu Arg Ser Pro His Met Asn Leu Ser Gly Thr Ala Glu Ser Leu
545 550 555 560

Asn Thr Val Ser Ile Thr Glu Tyr Glu Glu Glu Ser Leu Leu Thr Ser
565 570 575

Phe Lys Leu Asp Thr Gly Ala Glu Asp Ser Ser Gly Ser Ser Pro Ala
580 585 590

Thr Ser Ala Ile Pro Phe Ile Ser Glu Asn Ile Ser Gln Gly Tyr Ile
595 600 605

Phe Ser Ser Glu Asn Pro Glu Thr Ile Thr Tyr Asp Val Leu Ile Pro
610 615 620

Glu Ser Ala Arg Asn Ala Ser Glu Asp Ser Thr Ser Ser Gly Ser Glu
625 630 635 640

Phe Leu Gln Thr Asn Tyr Thr Glu Ile Arg Val Asp Glu Ser Glu Lys
675 680 685

Thr Thr Lys Ser Phe Ser Ala Gly Pro Val Met Ser Gln Gly Pro Ser
690 695 700

Val Thr Asp Leu Glu Met Pro His Tyr Ser Thr Phe Ala Tyr Phe Pro
705 710 715 720

Thr Glu Val Thr Pro His Ala Phe Thr Pro Ser Ser Arg Gln Gln Asp
725 730 735

Leu Val Ser Thr Val Asn Val Val Tyr Ser Gln Thr Thr Gln Pro Val
740 745 750

Tyr Asn Gly Glu Thr Pro Leu Gln Pro Ser Tyr Ser Ser Glu Val Phe
755 760 765

Pro Leu Val Thr Pro Leu Leu Leu Asp Asn Gln Ile Leu Asn Thr Thr
770 775 780

Pro Ala Ala Ser Ser Ser Asp Ser Ala Leu His Ala Thr Pro Val Phe
785 790 795 800

Pro Ser Val Asp Val Ser Phe Glu Ser Ile Leu Ser Ser Tyr Asp Gly
805 810 815

Ala Pro Leu Leu Pro Phe Ser Ser Ala Ser Phe Ser Ser Glu Leu Phe
820 825 830

Asn His Leu His Thr Val Ser Gln Ile Leu His Gln Val Thr Ser Ala
835 840 845

Thr Glu Ser Asp Lys Val Pro Leu His Ala Ser Leu Pro Val Ala Gly
850 855 860

Gly Asp Leu Leu Leu Glu Pro Ser Leu Ala Gln Tyr Ser Asp Val Leu

Gly Val Leu Tyr Lys Thr Leu Met Phe Ser Gln Val Glu Pro Pro Ser
900 905 910

Ser Asp Ala Met Met His Ala Arg Ser Ser Gly Pro Glu Pro Ser Tyr
915 920 925

Ala Leu Ser Asp Asn Glu Gly Ser Gln His Ile Phe Thr Val Ser Tyr
930 935 940

Ser Ser Ala Ile Pro Val His Asp Ser Val Gly Val Thr Tyr Gln Gly
945 950 955 960

Ser Leu Phe Ser Gly Pro Ser His Ile Pro Ile Pro Lys Ser Ser Leu
965 970 975

Ile Thr Pro Thr Ala Ser Leu Leu Gln Pro Thr His Ala Leu Ser Gly
980 985 990

Asp Gly Glu Trp Ser Gly Ala Ser Ser Asp Ser Glu Phe Leu Leu Pro
995 1000 1005

Asp Thr Asp Gly Leu Thr Ala Leu Asn Ile Ser Ser Pro Val Ser
1010 1015 1020

Val Ala Glu Phe Thr Tyr Thr Thr Ser Val Phe Gly Asp Asp Asn
1025 1030 1035

Lys Ala Leu Ser Lys Ser Glu Ile Ile Tyr Gly Asn Glu Thr Glu
1040 1045 1050

Leu Gln Ile Pro Ser Phe Asn Glu Met Val Tyr Pro Ser Glu Ser
1055 1060 1065

Thr Val Met Pro Asn Met Tyr Asp Asn Val Asn Lys Leu Asn Ala
1070 1075 1080

Ser Leu Gln Glu Thr Ser Val Ser Ile Ser Ser Thr Lys Gly Met
1085 1090 1095

Glu Ile Ser Gln Val Pro Glu Asn Asn Phe Ser Val Gln Pro Thr
1115 1120 1125

His Thr Val Ser Gln Ala Ser Gly Asp Thr Ser Leu Lys Pro Val
1130 1135 1140

Leu Ser Ala Asn Ser Glu Pro Ala Ser Ser Asp Pro Ala Ser Ser
1145 1150 1155

Glu Met Leu Ser Pro Ser Thr Gln Leu Leu Phe Tyr Glu Thr Ser
1160 1165 1170

Ala Ser Phe Ser Thr Glu Val Leu Leu Gln Pro Ser Phe Gln Ala
1175 1180 1185

Ser Asp Val Asp Thr Leu Leu Lys Thr Val Leu Pro Ala Val Pro
1190 1195 1200

Ser Asp Pro Ile Leu Val Glu Thr Pro Lys Val Asp Lys Ile Ser
1205 1210 1215

Ser Thr Met Leu His Leu Ile Val Ser Asn Ser Ala Ser Ser Glu
1220 1225 1230

Asn Met Leu His Ser Thr Ser Val Pro Val Phe Asp Val Ser Pro
1235 1240 1245

Thr Ser His Met His Ser Ala Ser Leu Gln Gly Leu Thr Ile Ser
1250 1255 1260

Tyr Ala Ser Glu Lys Tyr Glu Pro Val Leu Leu Lys Ser Glu Ser
1265 1270 1275

Ser His Gln Val Val Pro Ser Leu Tyr Ser Asn Asp Glu Leu Phe
1280 1285 1290

Gln Thr Ala Asn Leu Glu Ile Asn Gln Ala His Pro Pro Lys Gly
1295 1300 1305

Asn Thr Val Ser Asn Asp Ser Thr His Ser Asp Val Thr Thr Thr

1325		1330		1335
Ser Thr Lys Ser Ser Val Thr Gly Lys Val Phe Ala Gly Ile Pro				
1340		1345		1350
Thr Val Ala Ser Asp Thr Phe Val Ser Thr Asp His Ser Val Pro				
1355		1360		1365
Ile Gly Asn Gly His Val Ala Ile Thr Ala Val Ser Pro His Arg				
1370		1375		1380
Asp Gly Ser Val Thr Ser Thr Lys Leu Leu Phe Pro Ser Lys Ala				
1385		1390		1395
Thr Ser Glu Leu Ser His Ser Ala Lys Ser Asp Ala Gly Leu Val				
1400		1405		1410
Gly Gly Gly Glu Asp Gly Asp Thr Asp Asp Asp Gly Asp Asp Asp				
1415		1420		1425
Asp Asp Arg Asp Ser Asp Gly Leu Ser Ile His Lys Cys Met Ser				
1430		1435		1440
Cys Ser Ser Tyr Arg Glu Ser Gln Glu Lys Val Met Asn Asp Ser				
1445		1450		1455
Asp Thr His Glu Asn Ser Leu Met Asp Gln Asn Asn Pro Ile Ser				
1460		1465		1470
Tyr Ser Leu Ser Glu Asn Ser Glu Glu Asp Asn Arg Val Thr Ser				
1475		1480		1485
Val Ser Ser Asp Ser Gln Thr Gly Met Asp Arg Ser Pro Gly Lys				
1490		1495		1500
Ser Pro Ser Ala Asn Gly Leu Ser Gln Lys His Asn Asp Gly Lys				
1505		1510		1515

Gly Ser Gly Gln Gly Thr Ser Asp Ser Leu Asn Glu Asn Glu Thr
1550 1555 1560

Ser Thr Asp Phe Ser Phe Ala Asp Thr Asn Glu Lys Asp Ala Asp
1565 1570 1575

Gly Ile Leu Ala Ala Gly Asp Ser Glu Ile Thr Pro Gly Phe Pro
1580 1585 1590

Gln Ser Pro Thr Ser Ser Val Thr Ser Glu Asn Ser Glu Val Phe
1595 1600 1605

His Val Ser Glu Ala Glu Ala Ser Asn Ser Ser His Glu Ser Arg
1610 1615 1620

Ile Gly Leu Ala Glu Gly Leu Glu Ser Glu Lys Lys Ala Val Ile
1625 1630 1635

Pro Leu Val Ile Val Ser Ala Leu Thr Phe Ile Cys Leu Val Val
1640 1645 1650

Leu Val Gly Ile Leu Ile Tyr Trp Arg Lys Cys Phe Gln Thr Ala
1655 1660 1665

His Phe Tyr Leu Glu Asp Ser Thr Ser Pro Arg Val Ile Ser Thr
1670 1675 1680

Pro Pro Thr Pro Ile Phe Pro Ile Ser Asp Asp Val Gly Ala Ile
1685 1690 1695

Pro Ile Lys His Phe Pro Lys His Val Ala Asp Leu His Ala Ser
1700 1705 1710

Ser Gly Phe Thr Glu Glu Phe Glu Thr Leu Lys Glu Phe Tyr Gln
1715 1720 1725

Gln Val Gln Ser Cys Thr Val Asp Leu Glu Ile Thr Ala Asp Ser

Val Ala Tyr Asp His Ser Arg Val Lys Leu Ala Gln Leu Ala Glu
1760 1765 1770

Lys Asp Gly Lys Leu Thr Asp Tyr Ile Asn Ala Asn Tyr Val Asp
1775 1780 1785

Gly Tyr Asn Arg Pro Lys Ala Tyr Ile Ala Ala Gln Gly Pro Leu
1790 1795 1800

Lys Ser Thr Ala Glu Asp Phe Trp Arg Met Ile Trp Glu His Asn
1805 1810 1815

Val Glu Val Ile Val Met Ile Thr Asn Leu Val Glu Lys Gly Arg
1820 1825 1830

Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly Ser Glu Glu Tyr
1835 1840 1845

Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val Leu Ala Tyr
1850 1855 1860

Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile Lys Lys
1865 1870 1875

Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln Tyr
1880 1885 1890

His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu
1895 1900 1905

Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His
1910 1915 1920

Ala Val Gly Pro Val Val Val His Cys Ser Ala Gly Val Gly Arg
1925 1930 1935

Thr Gly Thr Tyr Ile Val Leu Asp Ser Met Leu Gln Gln Ile Gln
1940 1945 1950

Ser Gln Arg Asn Tyr Leu Val Gln Thr Glu Glu Gln Tyr Val Phe
1970 1975 1980

Ile His Asp Thr Leu Val Glu Ala Ile Leu Ser Lys Glu Thr Glu
1985 1990 1995

Val Leu Asp Ser His Ile His Ala Tyr Val Asn Ala Leu Leu Ile
2000 2005 2010

Pro Gly Pro Ala Gly Lys Thr Lys Leu Glu Lys Gln Phe Gln Gly
2015 2020 2025

Leu Thr Leu Ser Pro Arg Leu Glu Cys Arg Gly Thr Ile Ser Ala
2030 2035 2040

His Cys Asn Leu Pro Leu Pro Gly Leu Thr Asp Pro Pro Thr Ser
2045 2050 2055

Ala Ser Arg Val Ala Gly Thr Ile Leu Leu Ser Gln Ser Asn Ile
2060 2065 2070

Gln Gln Ser Asp Tyr Ser Ala Ala Leu Lys Gln Cys Asn Arg Glu
2075 2080 2085

Lys Asn Arg Thr Ser Ser Ile Ile Pro Val Glu Arg Ser Arg Val
2090 2095 2100

Gly Ile Ser Ser Leu Ser Gly Glu Gly Thr Asp Tyr Ile Asn Ala
2105 2110 2115

Ser Tyr Ile Met Gly Tyr Tyr Gln Ser Asn Glu Phe Ile Ile Thr
2120 2125 2130

Gln His Pro Leu Leu His Thr Ile Lys Asp Phe Trp Arg Met Ile
2135 2140 2145

Trp Asp His Asn Ala Gln Leu Val Val Met Ile Pro Asp Gly Gln
2150 2155 2160

2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 2275 2280 2285 2290 2295 2300 2305 2310 2315 2320 2325 2330 2335 2340 2345 2350 2355 2360 2365 2370 2375 2380 2385 2390 2395 2400 2405 2410 2415 2420 2425 2430 2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485 2490 2495 2500 2505 2510 2515 2520 2525 2530 2535 2540 2545 2550 2555 2560 2565 2570 2575 2580 2585 2590 2595 2600 2605 2610 2615 2620 2625 2630 2635 2640 2645 2650 2655 2660 2665 2670 2675 2680 2685 2690 2695 2700 2705 2710 2715 2720 2725 2730 2735 2740 2745 2750 2755 2760 2765 2770 2775 2780 2785 2790 2795 2800 2805 2810 2815 2820 2825 2830 2835 2840 2845 2850 2855 2860 2865 2870 2875 2880 2885 2890 2895 2900 2905 2910 2915 2920 2925 2930 2935 2940 2945 2950 2955 2960 2965 2970 2975 2980 2985 2990 2995 3000 3005 3010 3015 3020 3025 3030 3035 3040 3045 3050 3055 3060 3065 3070 3075 3080 3085 3090 3095 3100 3105 3110 3115 3120 3125 3130 3135 3140 3145 3150 3155 3160 3165 3170 3175 3180 3185 3190 3195 3200 3205 3210 3215 3220 3225 3230 3235 3240 3245 3250 3255 3260 3265 3270 3275 3280 3285 3290 3295 3300 3305 3310 3315 3320 3325 3330 3335 3340 3345 3350 3355 3360 3365 3370 3375 3380 3385 3390 3395 3400 3405 3410 3415 3420 3425 3430 3435 3440 3445 3450 3455 3460 3465 3470 3475 3480 3485 3490 3495 3500 3505 3510 3515 3520 3525 3530 3535 3540 3545 3550 3555 3560 3565 3570 3575 3580 3585 3590 3595 3600 3605 3610 3615 3620 3625 3630 3635 3640 3645 3650 3655 3660 3665 3670 3675 3680 3685 3690 3695 3700 3705 3710 3715 3720 3725 3730 3735 3740 3745 3750 3755 3760 3765 3770 3775 3780 3785 3790 3795 3800 3805 3810 3815 3820 3825 3830 3835 3840 3845 3850 3855 3860 3865 3870 3875 3880 3885 3890 3895 3900 3905 3910 3915 3920 3925 3930 3935 3940 3945 3950 3955 3960 3965 3970 3975 3980 3985 3990 3995 4000 4005 4010 4015 4020 4025 4030 4035 4040 4045 4050 4055 4060 4065 4070 4075 4080 4085 4090 4095 4100 4105 4110 4115 4120 4125 4130 4135 4140 4145 4150 4155 4160 4165 4170 4175 4180 4185 4190 4195 4200 4205 4210 4215 4220 4225 4230 4235 4240 4245 4250 4255 4260 4265 4270 4275 4280 4285 4290 4295 4300 4305 4310 4315 4320 4325 4330 4335 4340 4345 4350 4355 4360 4365 4370 4375 4380 4385 4390 4395 4400 4405 4410 4415 4420 4425 4430 4435 4440 4445 4450 4455 4460 4465 4470 4475 4480 4485 4490 4495 4500 4505 4510 4515 4520 4525 4530 4535 4540 4545 4550 4555 4560 4565 4570 4575 4580 4585 4590 4595 4600 4605 4610 4615 4620 4625 4630 4635 4640 4645 4650 4655 4660 4665 4670 4675 4680 4685 4690 4695 4700 4705 4710 4715 4720 4725 4730 4735 4740 4745 4750 4755 4760 4765 4770 4775 4780 4785 4790 4795 4800 4805 4810 4815 4820 4825 4830 4835 4840 4845 4850 4855 4860 4865 4870 4875 4880 4885 4890 4895 4900 4905 4910 4915 4920 4925 4930 4935 4940 4945 4950 4955 4960 4965 4970 4975 4980 4985 4990 4995 5000 5005 5010 5015 5020 5025 5030 5035 5040 5045 5050 5055 5060 5065 5070 5075 5080 5085 5090 5095 5100 5105 5110 5115 5120 5125 5130 5135 5140 5145 5150 5155 5160 5165 5170 5175 5180 5185 5190 5195 5200 5205 5210 5215 5220 5225 5230 5235 5240 5245 5250 5255 5260 5265 5270 5275 5280 5285 5290 5295 5300 5305 5310 5315 5320 5325 5330 5335 5340 5345 5350 5355 5360 5365 5370 5375 5380 5385 5390 5395 5400 5405 5410 5415 5420 5425 5430 5435 5440 5445 5450 5455 5460 5465 5470 5475 5480 5485 5490 5495 5500 5505 5510 5515 5520 5525 5530 5535 5540 5545 5550 5555 5560 5565 5570 5575 5580 5585 5590 5595 5600 5605 5610 5615 5620 5625 5630 5635 5640 5645 5650 5655 5660 5665 5670 5675 5680 5685 5690 5695 5700 5705 5710 5715 5720 5725 5730 5735 5740 5745 5750 5755 5760 5765 5770 5775 5780 5785 5790 5795 5800 5805 5810 5815 5820 5825 5830 5835 5840 5845 5850 5855 5860 5865 5870 5875 5880 5885 5890 5895 5900 5905 5910 5915 5920 5925 5930 5935 5940 5945 5950 5955 5960 5965 5970 5975 5980 5985 5990 5995 6000 6005 6010 6015 6020 6025 6030 6035 6040 6045 6050 6055 6060 6065 6070 6075 6080 6085 6090 6095 6100 6105 6110 6115 6120 6125 6130 6135 6140 6145 6150 6155 6160 6165 6170 6175 6180 6185 6190 6195 6200 6205 6210 6215 6220 6225 6230 6235 6240 6245 6250 6255 6260 6265 6270 6275 6280 6285 6290 6295 6300 6305 6310 6315 6320 6325 6330 6335 6340 6345 6350 6355 6360 6365 6370 6375 6380 6385 6390 6395 6400 6405 6410 6415 6420 6425 6430 6435 6440 6445 6450 6455 6460 6465 6470 6475 6480 6485 6490 6495 6500 6505 6510 6515 6520 6525 6530 6535 6540 6545 6550 6555 6560 6565 6570 6575 6580 6585 6590 6595 6600 6605 6610 6615 6620 6625 6630 6635 6640 6645 6650 6655 6660 6665 6670 6675 6680 6685 6690 6695 6700 6705 6710 6715 6720 6725 6730 6735 6740 6745 6750 6755 6760 6765 6770 6775 6780 6785 6790 6795 6800 6805 6810 6815 6820 6825 6830 6835 6840 6845 6850 6855 6860 6865 6870 6875 6880 6885 6890 6895 6900 6905 6910 6915 6920 6925 6930 6935 6940 6945 6950 6955 6960 6965 6970 6975 6980 6985 6990 6995 7000 7005 7010 7015 7020 7025 7030 7035 7040 7045 7050 7055 7060 7065 7070 7075 7080 7085 7090 7095 7100 7105 7110 7115 7120 7125 7130 7135 7140 7145 7150 7155 7160 7165 7170 7175 7180 7185 7190 7195 7200 7205 7210 7215 7220 7225 7230 7235 7240 7245 7250 7255 7260 7265 7270 7275 7280 7285 7290 7295 7300 7305 7310 7315 7320 7325 7330 7335 7340 7345 7350 7355 7360 7365 7370 7375 7380 7385 7390 7395 7400 7405 7410 7415 7420 7425 7430 7435 7440 7445 7450 7455 7460 7465 7470 7475 7480 7485 7490 7495 7500 7505 7510 7515 7520 7525 7530 7535 7540 7545 7550 7555 7560 7565 7570 7575 7580 7585 7590 7595 7600 7605 7610 7615 7620 7625 7630 7635 7640 7645 7650 7655 7660 7665 7670 7675 7680 7685 7690 7695 7700 7705 7710 7715 7720 7725 7730 7735 7740 7745 7750 7755 7760 7765 7770 7775 7780 7785 7790 7795 7800 7805 7810 7815 7820 7825 7830 7835 7840 7845 7850 7855 7860 7865 7870 7875 7880 7885 7890 7895 7900 7905 7910 7915 7920 7925 7930 7935 7940 7945 7950 7955 7960 7965 7970 7975 7980 7985 7990 7995 8000 8005 8010 8015 8020 8025 8030 8035 8040 8045 8050 8055 8060 8065 8070 8075 8080 8085 8090 8095 8100 8105 8110 8115 8120 8125 8130 8135 8140 8145 8150 8155 8160 8165 8170 8175 8180 8185 8190 8195 8200 8205 8210 8215 8220 8225 8230 8235 8240 8245 8250 8255 8260 8265 8270 8275 8280 8285 8290 8295 8300 8305 8310 8315 8320 8325 8330 8335 8340 8345 8350 8355 8360 8365 8370 8375 8380 8385 8390 8395 8400 8405 8410 8415 8420 8425 8430 8435 8440 8445 8450 8455 8460 8465 8470 8475 8480 8485 8490 8495 8500 8505 8510 8515 8520 8525 8530 8535 8540 8545 8550 8555 8560 8565 8570 8575 8580 8585 8590 8595 8600 8605 8610 8615 8620 8625 8630 8635 8640 8645 8650 8655 8660 8665 8670 8675 8680 8685 8690 8695 8700 8705 8710 8715 8720 8725 8730 8735 8740 8745 8750 8755 8760 8765 8770 8775 8780 8785 8790 8795 8800 8805 8810 8815 8820 8825 8830 8835 8840 8845 8850 8855 8860 8865 8870 8875 8880 8885 8890 8895 8900 8905 8910 8915 8920 8925 8930 8935 8940 8945 8950 8955 8960 8965 8970 8975 8980 8985 8990 8995 9000 9005 9010 9015 9020 9025 9030 9035 9040 9045 9050 9055 9060 9065 9070 9075 9080 9085 9090 9095 9100 9105 9110 9115 9120 9125 9130 9135 9140 9145 9150 9155 9160 9165 9170 9175 9180 9185 9190 9195 9200 9205 9210 9215 9220 9225 9230 9235 9240 9245 9250 9255 9260 9265 9270 9275 9280 9285 9290 9295 9300 9305 9310 9315 9320 9325 9330 9335 9340 9345 9350 9355 9360 9365 9370 9375 9380 9385 9390 9395 9400 9405 9410 9415 9420 9425 9430 9435 9440 9445 9450 9455 9460 9465 9470 9475 9480 9485 9490 9495 9500 9505 9510 9515 9520 9525 9530 9535 9540 9545 9550 9555 9560 9565 9570 9575 9580 9585 9590 9595 9600 9605 9610 9615 9620 9625 9630 9635 9640 9645 9650 9655 9660 9665 9670 9675 9680 9685 9690 9695 9700 9705 9710 9715 9720 9725 9730 9735 9740 9745 9750 9755 9760 9765 9770 9775 9780 9785 9790 9795 9800 9805 9810 9815 9820 9825 9830 9835 9840 9845 9850 9855 9860 9865 9870 9875 9880 9885 9890 9895 9900 9905 9910 9915 9920 9925 9930 9935 9940 9945 9950 9955 9960 9965 9970 9975 9980 9985 9990 9995 10000 10005 10010 10015 10020 10025 10030 10035 10040 10045 10050 10055 10060 10065 10070 10075 10080 10085 10090 10095 10100 10105 10110 10115 10120 10125 10130 10135 10140 10145 10150 10155 10160 10165 10170 10175 10180 10185 10190 10195 10200 10205 10210 10215 10220 10225 10230 10235 10240 10245 10250 10255 10260 10265 10270 10275 10280 10285 10290 10295 10300 10305 10310 10315 10320 10325 10330 10335 10340 10345 10350 10355 10360 10365 10370 10375 10380 10385 10390 10395 10400 10405 10410 10415 10420 10425 10430 10435 10440 10445 10450 10455 10460 10465 10470 10475 10480 10485 10490 10495 10500 10505 10510 10515 10520 10525 10530 10535 10540 10545 10550 10555 10560 10565 10570 10575 10580 10585 10590 10595 10600 10605 10610 10615 10620 10625 10630 10635 10640 10645 10650 10655 10660 10665 10670 10675 10680 10685 10690 10695 10700 10705 10710 10715 10720 10725 10730 10735 10740 10745 10750 10755 10760 10765 10770 10775 10780 10785 10790 10795 10800 10805 10810 10815 10820 10825 10830 10835 10840 10845 10850 10855 10860 10865 10870 10875 10880 10885 10890 10895 10900 10905 10910 10915 10920 10925 10930 10935 10940 10945 10950 10955 10960 10965 10970 10975 10980 10985 10990 10995 11000 11005 11010 11015 11020 11025 11030 11035 11040 11045 11050 11055 11060 11065 11070 11075 11080 11085 11090 11095 11100 11105 11110 11115 11120 11125 11130 11135 11140 11145 11150 11155 11160 11165 11170 11175 11180 11185 11190 11195 11200 11205 11210 11215 11220 11225 11230 11235 11240 11245 11250 11255 11260 11265 11270 11275 11280 11285 11290 11295 11300 11305 11310 11315 11320 11325 11330 11335 11340 11345 11350 11355 11360 11365 11370 11375 11380 11385 11390 11395 11400 11405 11410 11415 11420 11425 11430 11435 11440 11445 11450 11455 11460 11465 11470 11475 11480 11485 11490 11495 11500 11505 11510 11515 11520 11525 11530 11535 11540 11545 11550 11555 11560 11565 11570 11575 11580 11585 11590 11595 11600 11605 11610 11615 11620 11625 11630 11635 11640 11645 11650 11655 11660 11665 11670 11675 11680 11685 11690 11695 11700 11705 11710 11715 11720 11725 11730 11735 11740 11745 11750 11755 11760 11765 11770 11775 11780 11785 11790 11795 11800 11805 11810 11815 11820 11825 11830 11835 11840 11845 11850 11855 11860 11865 11870 11875 11880 11885 11890 11895 11900 11905 11910 11915 11920 11925 11930 11935 11940 11945 11950 11955 11960 11965 11970 11975 11980 11985 11990 11995 12000 12005 12010 12015 12020 12025 12030 12035 12040 12045 12050 12055 12060 12065 12070 12075 12080 12085 12090 12095 12100 12105 12110 12115 12120 12125 12130 12135 12140 12145 12150 12155 12160 12165 12170 12175 12180 12185 12190 12195 12200 12205 12210 12215 12220 12225 12230 12235 12240 12245 12250 12255 12260 12265 12270 12275 12280 12285 12290 12295 12300 12305 12310 12315 12320 12325 12330 12335 12340 12345 12350 12355 12360 12365 12370 12375 12380 12385 12390 12395 12400 12405 12410 12415 12420 12425 12430 12435 12440 12445 12450 12455 12460 12465 12470 12475 12480 12485 12490 12495 12500 12505 12510 12515 12520 12525 12530 12535 12540 12545 12550 12555 12560 12565 12570 12575 12580 12585 12590 12595 12600 12605 12610 12615 12620 12625 12630 12635 12640 12645 12650 12655 12660 12665 12670 12675 12680 12685 12690 12695 12700 12705 12710 12715 12720 12725 12730 12735 12740 12745 12750 12755 12760 12765 12770 12775 12780 12785 12790 12795 12800 12805 12810 12815 12820 12825 12830 12835 12840 12845 12850 12855 12860 12865 12870 12875 12880 12885 12890 12895 12900 12905 12910 12915 12920 12925 12930 12935 12940 12945 12950 12955 12960 12965 12970 12975 12980 12985 12990 12995 13000 13005 13010 13015

2180	2185	2190
His Lys Cys Leu Ser Asn Glu Glu Lys Leu Ile Ile Gln Asp Phe		
2195	2200	2205
Ile Leu Glu Ala Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His		
2210	2215	2220
Phe Gln Cys Pro Lys Trp Pro Asn Pro Asp Ser Pro Ile Ser Lys		
2225	2230	2235
Thr Phe Glu Leu Ile Ser Val Ile Lys Glu Glu Ala Ala Asn Arg		
2240	2245	2250
Asp Gly Pro Met Ile Val His Asp Glu His Gly Gly Val Thr Ala		
2255	2260	2265
Gly Thr Phe Cys Ala Leu Thr Thr Leu Met His Gln Leu Glu Lys		
2270	2275	2280
Glu Asn Ser Val Asp Val Tyr Gln Val Ala Lys Met Ile Asn Leu		
2285	2290	2295
Met Arg Pro Gly Val Phe Ala Asp Ile Glu Gln Tyr Gln Phe Leu		
2300	2305	2310
Tyr Lys Val Ile Leu Ser Leu Val Ser Thr Arg Gln Glu Glu Asn		
2315	2320	2325
Pro Ser Thr Ser Leu Asp Ser Asn Gly Ala Ala Leu Pro Asp Gly		
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Asn Ile Ala Glu Ser Leu Glu Ser Leu Val		
2345	2350	

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<223> PTP-zeta

15

[illegible]

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Gly Thr Glu Glu Asn Leu Asp Phe Lys Ala Ile Ile Asp Gly Val Glu	
190 195 200	
agt gtt agt cgt ttt ggg aag cag gct gct tta gat cca ttc ata ctg	798
Ser Val Ser Arg Phe Gly Lys Gln Ala Ala Leu Asp Pro Phe Ile Leu	
205 210 215	
ttg aac ctt ctg cca aac tca act gac aag tat tac att tac aat ggc	846
Leu Asn Leu Leu Pro Asn Ser Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly	
220 225 230	
tca ttg aca tct cct ccc tgc aca gac aca gtt gac tgg att gtt ttt	894
Ser Leu Thr Ser Pro Pro Cys Thr Asp Thr Val Asp Trp Ile Val Phe	
235 240 245	
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Lys Asp Thr Val Ser Ile Ser Glu Ser Gln Leu Ala Val Phe Cys Glu	
250 255 260 265	
gtt ctt aca atg caa caa tct ggt tat gtc atg ctg atg gac tac tta	990
Val Leu Thr Met Gln Gln Ser Gly Tyr Val Met Leu Met Asp Tyr Leu	
270 275 280	
caa aac aat ttt cga gag caa cag tac aag ttc tct aga cag gtg ttt	1038
Gln Asn Asn Phe Arg Glu Gln Gln Tyr Lys Phe Ser Arg Gln Val Phe	
285 290 295	
tcc tca tac act gga aag gaa gag att cat gaa gca gtt tgt agt tca	1086
Ser Ser Tyr Thr Gly Lys Glu Glu Ile His Glu Ala Val Cys Ser Ser	
300 305 310	
gaa cca gaa aat gtt cag gct gac cca gag aat tat acc agc ctt ctt	1134
Glu Pro Glu Asn Val Gln Ala Asp Pro Glu Asn Tyr Thr Ser Leu Leu	
315 320 325	
gtt aca tgg gaa aga cct cga gtc gtt tat gat acc atg att gag aag	1182
Val Thr Trp Glu Arg Pro Arg Val Val Tyr Asp Thr Met Ile Glu Lys	
330 335 340 345	
ttt gca gtt ttg tac cag cag ttg gat gga gag gac caa acc aag cat	1230
Phe Ala Val Leu Tyr Gln Gln Leu Asp Gly Glu Asp Gln Thr Lys His	
350 355 360	
gaa ttt ttg aca gat ggc tat caa gac ttg ggt gct att ctc aat aat	1278
Glu Phe Leu Thr Asp Gly Tyr Gln Asp Leu Gly Ala Ile Leu Asn Asn	
365 370 375	

Val Thr Trp Glu Arg Pro Arg Val Val Tyr Asp Thr Met Ile Glu Lys
 Asn Gly Leu Tyr Gly Lys Tyr Ser Arg Gln Leu Ile Val Asp Met Phe

395	400	405	
act gat aat cct gaa ctt gat ctt ttc cct gaa tta att gga act gaa			1422
Thr Asp Asn Pro Glu Leu Asp Leu Phe Pro Glu Leu Ile Gly Thr Glu			
410	415	420	425
gaa ata atc aag gag gag gaa gag gga aaa gac att gaa gaa ggc gct			1470
Glu Ile Ile Lys Glu Glu Glu Glu Gly Lys Asp Ile Glu Glu Gly Ala			
	430	435	440
att gtg aat cct ggt aga gac agt gct aca aac caa atc agg aaa aag			1518
Ile Val Asn Pro Gly Arg Asp Ser Ala Thr Asn Gln Ile Arg Lys Lys			
	445	450	455
gaa ccc cag att tct acc aca aca cac tac aat cgc ata ggg acg aaa			1566
Glu Pro Gln Ile Ser Thr Thr His Tyr Asn Arg Ile Gly Thr Lys			
	460	465	470
tac aat gaa gcc aag act aac cga tcc cca aca aga gga agt gaa ttc			1614
Tyr Asn Glu Ala Lys Thr Asn Arg Ser Pro Thr Arg Gly Ser Glu Phe			
	475	480	485
tct gga aag ggt gat gtt ccc aat aca tct tta aat tcc act tcc caa			1662
Ser Gly Lys Gly Asp Val Pro Asn Thr Ser Leu Asn Ser Thr Ser Gln			
490	495	500	505
cca gtc act aaa tta gcc aca gaa aaa gat att tcc ttg act tct cag			1710
Pro Val Thr Lys Leu Ala Thr Glu Lys Asp Ile Ser Leu Thr Ser Gln			
	510	515	520
act gtg act gaa ctg cca cct cac act gtg gaa ggt act tca gcc tct			1758
Thr Val Thr Glu Leu Pro Pro His Thr Val Glu Gly Thr Ser Ala Ser			
	525	530	535
tta aat gat ggc tct aaa act gtt ctt aga tct cca cat atg aac ttg			1806
Leu Asn Asp Gly Ser Lys Thr Val Leu Arg Ser Pro His Met Asn Leu			
	540	545	550
tcg ggg act gca gaa tcc tta aat aca gtt tct ata aca gaa tat gag			1854
Ser Gly Thr Ala Glu Ser Leu Asn Thr Val Ser Ile Thr Glu Tyr Glu			
	555	560	565
gag gag agt tta ttg acc agt ttc aag ctt gat act gga gct gaa gat			1902
Glu Glu Ser Leu Leu Thr Ser Phe Lys Leu Asp Thr Gly Ala Glu Asp			
570	575	580	585
tct tca ggc tcc agt ccc gca act tct gct atc cca ttc atc tct gag			1950
Ser Ser Gly Ser Ser Pro Ala Thr Ser Ala Ile Pro Phe Ile Ser Glu			
	590	595	600
aac ata ttc caa ggg tat ata ttt tcc tcc gaa aac cca gaa aca ata			1998

Thr Asp Arg Leu Ile Thr Pro Ala Val Ala Asn Asn Ala Val Thr Thr Arg
 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470

tca act tca tca ggt tca gaa gaa tca cta aag gat cct tct atg gag Ser Thr Ser Ser Gly Ser Glu Glu Ser Leu Lys Asp Pro Ser Met Glu 635 640 645	2094
gga aat gtg tgg ttt cct agc tct aca gac ata aca gca cag ccc gat Gly Asn Val Trp Phe Pro Ser Ser Thr Asp Ile Thr Ala Gln Pro Asp 650 655 660 665	2142
gtt gga tca ggc aga gag agc ttt ctc cag act aat tac act gag ata Val Gly Ser Gly Arg Glu Ser Phe Leu Gln Thr Asn Tyr Thr Glu Ile 670 675 680	2190
cgt gtt gat gaa tct gag aag aca acc aag tcc ttt tct gca ggc cca Arg Val Asp Glu Ser Glu Lys Thr Thr Lys Ser Phe Ser Ala Gly Pro 685 690 695	2238
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aat cag atc ctc aac act acc cct gct gct tca agt agt gat tcg gcc Asn Gln Ile Leu Asn Thr Thr Pro Ala Ala Ser Ser Ser Asp Ser Ala 780 785 790	2526
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atc ctg tct tcc tat gat ggt gca cct ttg ctt cca ttt tcc tct gct Ile Leu Ser Ser Tyr Asp Gly Ala Pro Leu Leu Pro Phe Ser Ser Ala 810 815 820 825	2622
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gct tct ctg cca gtg gct ggg ggt gat ttg cta tta gag ccc agc ctt Ala Ser Leu Pro Val Ala Gly Gly Asp Leu Leu Leu Glu Pro Ser Leu 860 865 870	2765
gct cag tat tct gat gtg ctg tcc act act cat gct gct tca gag acg Ala Gln Tyr Ser Asp Val Leu Ser Thr Thr His Ala Ala Ser Glu Thr 875 880 885	2814
ctg gaa ttt ggt agt gaa tct ggt gtt ctt tat aaa acg ctt atg ttt Leu Glu Phe Gly Ser Glu Ser Gly Val Leu Tyr Lys Thr Leu Met Phe 890 895 900 905	2862
tct caa gtt gaa cca ccc agc agt gat gcc atg atg cat gca cgt tct Ser Gln Val Glu Pro Pro Ser Ser Asp Ala Met Met His Ala Arg Ser 910 915 920	2910
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cac atc ttc act gtt tct tac agt tct gca ata cct gtg cat gat tct His Ile Phe Thr Val Ser Tyr Ser Ser Ala Ile Pro Val His Asp Ser 940 945 950	3006
gtg ggt gta act tat cag ggt tcc tta ttt agc ggc cct agc cat ata Val Gly Val Thr Tyr Gln Gly Ser Leu Phe Ser Gly Pro Ser His Ile 955 960 965	3054
cca ata cct aag tct tcg tta ata acc cca act gca tca tta ctg cag Pro Ile Pro Lys Ser Ser Leu Ile Thr Pro Thr Ala Ser Leu Leu Gln 970 975 980 985	3102
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aac att tct tca cct gtt tct gta gct gaa ttt aca tat aca aca Asn Ile Ser Ser Pro Val Ser Val Ala Glu Phe Thr Tyr Thr Thr 1020 1025 1030	3240
tct gtg ttt ggt gat gat aat aag gcg ctt tct aaa agt gaa ata Ser Val Phe Gly Asp Asp Asn Lys Ala Leu Ser Lys Ser Glu Ile 1035 1040 1045	3285
ata tat gga aat gag act gaa ctg caa att cct tct ttc aat gag Ile Tyr Gly Asn Glu Thr Glu Leu Gln Ile Pro Ser Phe Asn Glu 1050 1055 1060	3330

atg ata ttt ttt ttt act ggt ttt tta tta tta act ttt gtt ttt 341

Asn Val Asn Lys	Leu Asn Ala Ser	Leu Gln Glu Thr Ser Val Ser	
1080		1085	1090
att tct agc acc	aag ggc atg ttt cca	ggg tcc ctt gct cat acc	3465
Ile Ser Ser Thr	Lys Gly Met Phe Pro	Gly Ser Leu Ala His Thr	
1095	1100	1105	
acc act aag gtt	ttt gat cat gag att	agt caa gtt cca gaa aat	3510
Thr Thr Lys Val	Phe Asp His Glu Ile	Ser Gln Val Pro Glu Asn	
1110	1115	1120	
aac ttt tca gtt	caa cct aca cat act	gtc tct caa gca tct ggt	3555
Asn Phe Ser Val	Gln Pro Thr His Thr	Val Ser Gln Ala Ser Gly	
1125	1130	1135	
gac act tgc ctt	aaa cct gtg ctt agt	gca aac tca gag cca gca	3600
Asp Thr Ser Leu	Lys Pro Val Leu Ser	Ala Asn Ser Glu Pro Ala	
1140	1145	1150	
tcc tct gac cct	gct tct agt gaa atg	tta tct cct tca act cag	3645
Ser Ser Asp Pro	Ala Ser Ser Glu Met	Leu Ser Pro Ser Thr Gln	
1155	1160	1165	
ctc tta ttt tat	gag acc tca gct tct	ttt agt act gaa gta ttg	3690
Leu Leu Phe Tyr	Glu Thr Ser Ala Ser	Phe Ser Thr Glu Val Leu	
1170	1175	1180	
cta caa cct tcc	ttt cag gct tct gat	gtt gac acc ttg ctt aaa	3735
Leu Gln Pro Ser	Phe Gln Ala Ser Asp	Val Asp Thr Leu Leu Lys	
1185	1190	1195	
act gtt ctt cca	gct gtg ccc agt gat	cca ata ttg gtt gaa acc	3780
Thr Val Leu Pro	Ala Val Pro Ser Asp	Pro Ile Leu Val Glu Thr	
1200	1205	1210	
ccc aaa gtt gat	aaa att agt tct aca	atg ttg cat ctc att gta	3825
Pro Lys Val Asp	Lys Ile Ser Ser Thr	Met Leu His Leu Ile Val	
1215	1220	1225	
tca aat tct gct	tca agt gaa aac atg	ctg cac tct aca tct gta	3870
Ser Asn Ser Ala	Ser Ser Glu Asn Met	Leu His Ser Thr Ser Val	
1230	1235	1240	
cca gtt ttt gat	gtg tgc cct act tct	cat atg cac tct gct tca	3915
Pro Val Phe Asp	Val Ser Pro Thr Ser	His Met His Ser Ala Ser	
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ctt caa ggt ttg	acc att tcc tat gca	agt gag aaa tat gaa cca	3960
Leu Gln Gly Leu	Thr Ile Ser Tyr Ala	Ser Glu Lys Tyr Glu Pro	
1260	1265	1270	

1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000 2005 2010 2015 2020 2025 2030 2035 2040 2045 2050 2055 2060 2065 2070 2075 2080 2085 2090 2095 2100 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 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Gln Ala His Pro Pro Lys Gly Arg His Val Phe Ala Thr Pro Val			
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Leu Ser Ile Asp Glu Pro Leu Asn Thr Leu Ile Asn Lys Leu Ile			
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cat tcc gat gaa att tta acc tcc acc aaa agt tct gtt act ggt			4185
His Ser Asp Glu Ile Leu Thr Ser Thr Lys Ser Ser Val Thr Gly			
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aag gta ttt gct ggt att cca aca gtt gct tct gat aca ttt gta			4230
Lys Val Phe Ala Gly Ile Pro Thr Val Ala Ser Asp Thr Phe Val			
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tct act gat cat tct gtt cct ata gga aat ggg cat gtt gcc att			4275
Ser Thr Asp His Ser Val Pro Ile Gly Asn Gly His Val Ala Ile			
1365	1370	1375	
aca gct gtt tct ccc cac aga gat ggt tct gta acc tca aca aag			4320
Thr Ala Val Ser Pro His Arg Asp Gly Ser Val Thr Ser Thr Lys			
1380	1385	1390	
ttg ctg ttt cct tct aag gca act tct gag ctg agt cat agt gcc			4365
Leu Leu Phe Pro Ser Lys Ala Thr Ser Glu Leu Ser His Ser Ala			
1395	1400	1405	
aaa tct gat gcc ggt tta gtg ggt ggt ggt gaa gat ggt gac act			4410
Lys Ser Asp Ala Gly Leu Val Gly Gly Gly Glu Asp Gly Asp Thr			
1410	1415	1420	
gat gat gat ggt gat gat gat gat gac aga gat agt gat ggc tta			4455
Asp Asp Asp Gly Asp Asp Asp Asp Asp Arg Asp Ser Asp Gly Leu			
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tcc att cat aag tgt atg tca tgc tca tcc tat aga gaa tca cag			4500
Ser Ile His Lys Cys Met Ser Cys Ser Ser Tyr Arg Glu Ser Gln			
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gaa aag gta atg aat gat tca gac acc cac gaa aac agt ctt atg			4545
Glu Lys Val Met Asn Asp Ser Asp Thr His Glu Asn Ser Leu Met			
1455	1460	1465	
gat cag aat aat cca atc tca tac tca cta tct gag aat tct gaa			4590
Asp Gln Asn Asn Pro Ile Ser Tyr Ser Leu Ser Glu Asn Ser Glu			
1470	1475	1480	
gaa gat aat aqa gtc aca agt ata tcc tca gac agt caa act ggt			4635

caa aag cac aat gat gga aaa gag gaa aat gac att cag act ggt	4725
Gln Lys His Asn Asp Gly Lys Glu Glu Asn Asp Ile Gln Thr Gly	
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Ser Ala Leu Leu Pro Leu Ser Pro Glu Ser Lys Ala Trp Ala Val	
1530 1535 1540	
ctg aca agt gat gaa gaa agt gga tca ggg caa ggt acc tca gat	4815
Leu Thr Ser Asp Glu Glu Ser Gly Ser Gly Gln Gly Thr Ser Asp	
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agc ctt aat gag aat gag act tcc aca gat ttc agt ttt gca gac	4860
Ser Leu Asn Glu Asn Glu Thr Ser Thr Asp Phe Ser Phe Ala Asp	
1560 1565 1570	
act aat gaa aaa gat gct gat ggg atc ctg gca gca ggt gac tca	4905
Thr Asn Glu Lys Asp Ala Asp Gly Ile Leu Ala Ala Gly Asp Ser	
1575 1580 1585	
gaa ata act cct gga ttc cca cag tcc cca aca tca tct gtt act	4950
Glu Ile Thr Pro Gly Phe Pro Gln Ser Pro Thr Ser Ser Val Thr	
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Asn Ser Ser His Glu Ser Arg Ile Gly Leu Ala Glu Gly Leu Glu	
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tcc gag aag aag gca gtt ata ccc ctt gtg atc gtg tca gcc ctg	5085
Ser Glu Lys Lys Ala Val Ile Pro Leu Val Ile Val Ser Ala Leu	
1635 1640 1645	
act ttt atc tgt cta gtg gtt ctt gtg ggt att ctc atc tac tgg	5130
Thr Phe Ile Cys Leu Val Val Leu Val Gly Ile Leu Ile Tyr Trp	
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agg aaa tgc ttc cag act gca cac ttt tac tta gag gat agt aca	5175
Arg Lys Cys Phe Gln Thr Ala His Phe Tyr Leu Glu Asp Ser Thr	
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tcc cct aga gtt ata tcc aca cct cca aca cct atc ttt cca att	5220
Ser Pro Arg Val Ile Ser Thr Pro Pro Thr Pro Ile Phe Pro Ile	
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tca gat gat gtc gga gca att cca ata aag cac ttt cca aag cat	5265
Ser Asp Asp Val Gly Ala Ile Pro Ile Lys His Phe Pro Lys His	

aca ctg aaa gag	ttt tac cag gaa gtg	cag agc tgt act gtt	gac	5355
Thr Leu Lys Glu	Phe Tyr Gln Glu Val	Gln Ser Cys Thr Val	Asp	
1725	1730	1735		
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Leu Gly Ile Thr	Ala Asp Ser Ser Asn	His Pro Asp Asn Lys	His	
1740	1745	1750		
aag aat cga tac	ata aat atc gtt gcc	tat gat cat agc agg	gtt	5445
Lys Asn Arg Tyr	Ile Asn Ile Val Ala	Tyr Asp His Ser Arg	Val	
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Lys Leu Ala Gln	Leu Ala Glu Lys Asp	Gly Lys Leu Thr Asp	Tyr	
1770	1775	1780		
atc aat gcc aat	tat gtt gat ggc tac	aac aga cca aaa gct	tat	5535
Ile Asn Ala Asn	Tyr Val Asp Gly Tyr	Asn Arg Pro Lys Ala	Tyr	
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att gct gcc caa	ggc cca ctg aaa tcc	aca gct gaa gat ttc	tgg	5580
Ile Ala Ala Gln	Gly Pro Leu Lys Ser	Thr Ala Glu Asp Phe	Trp	
1800	1805	1810		
aga atg ata tgg	gaa cat aat gtg gaa	gtt att gtc atg ata	aca	5625
Arg Met Ile Trp	Glu His Asn Val Glu	Val Ile Val Met Ile	Thr	
1815	1820	1825		
aac ctc gtg gag	aaa gga agg aga aaa	tgt gat cag tac tgg	cct	5670
Asn Leu Val Glu	Lys Gly Arg Arg Lys	Cys Asp Gln Tyr Trp	Pro	
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gcc gat ggg agt	gag gag tac ggg aac	ttt ctg gtc act cag	aag	5715
Ala Asp Gly Ser	Glu Glu Tyr Gly Asn	Phe Leu Val Thr Gln	Lys	
1845	1850	1855		
agt gtg caa gtg	ctt gcc tat tat act	gtg agg aat ttt act	cta	5760
Ser Val Gln Val	Leu Ala Tyr Tyr Thr	Val Arg Asn Phe Thr	Leu	
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aga aac aca aaa	ata aaa aag ggc tcc	cag aaa gga aga ccc	agt	5805
Arg Asn Thr Lys	Ile Lys Lys Gly Ser	Gln Lys Gly Arg Pro	Ser	
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gga cgt gtg gtc	aca cag tat cac tac	acg cag tgg cct gac	atg	5850
Gly Arg Val Val	Thr Gln Tyr His Tyr	Thr Gln Trp Pro Asp	Met	
1890	1895	1900		
gga gta cca gag	tac tcc ctg cca gtg	ctg acc ttt gtg aga	aag	5895
Gly Val Pro Glu	Tyr Ser Leu Pro Val	Leu Thr Phe Val Arg	Lys	
1905	1910	1915		

2145	2150	2155		
tgt cta tct aat	gag gaa aaa ctt	ata att cag gac ttt atc tta	6650	
Cys Leu Ser Asn	Glu Glu Lys Leu	Ile Ile Gln Asp Phe Ile Leu		
2160	2165	2170		
gaa gct aca cag	gat gat tat gta ctt	gaa gtg agg cac ttt cag	6705	
Glu Ala Thr Gln	Asp Asp Tyr Val	Leu Glu Val Arg His Phe Gln		
2175	2180	2185		
tgt cct aaa tgg	cca aat cca gat agc	ccc att agt aaa act ttt	6750	
Cys Pro Lys Trp	Pro Asn Pro Asp Ser	Pro Ile Ser Lys Thr Phe		
2190	2195	2200		
gaa ctt ata agt	gtt ata aaa gaa gaa	gct gcc aat agg gat ggg	6795	
Glu Leu Ile Ser	Val Ile Lys Glu Glu	Ala Ala Asn Arg Asp Gly		
2205	2210	2215		
cct atg att gtt	cat gat gag cat gga	gga gtg acg gca gga act	6840	
Pro Met Ile Val	His Asp Glu His Gly	Gly Val Thr Ala Gly Thr		
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ttc tgt gct ctg	aca acc ctt atg cac	caa cta gaa aaa gaa aat	6885	
Phe Cys Ala Leu	Thr Thr Leu Met His	Gln Leu Glu Lys Glu Asn		
2235	2240	2245		
tcc gtg gat gtt	tac cag gta gcc aag	atg atc aat ctg atg agg	6930	
Ser Val Asp Val	Tyr Gln Val Ala Lys	Met Ile Asn Leu Met Arg		
2250	2255	2260		
cca gga gtc ttt	gct gac att gag cag	tat cag ttt ctc tac aaa	6975	
Pro Gly Val Phe	Ala Asp Ile Glu Gln	Tyr Gln Phe Leu Tyr Lys		
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Val Ile Leu Ser	Leu Val Ser Thr Arg	Gln Glu Glu Asn Pro Ser		
2280	2285	2290		
acc tct ctg gac	agt aat ggt gca gca	ttg cct gat gga aat ata	7065	
Thr Ser Leu Asp	Ser Asn Gly Ala Ala	Leu Pro Asp Gly Asn Ile		
2295	2300	2305		
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Ala Glu Ser Leu	Glu Ser Leu Val			
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<222> (587)..(587)
<223> Chondroitin Sulfate (potential)

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 <223> Chondroitin sulfate (potential)

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 <223> Glycosylation; N-linked (GLCNAC...) (potential)

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<222> (2222)..(2222)

<223> Ancestral active site

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<101> Krueger, N.K. and Saito, H.

<102> A human transmembrane protein-tyrosine-phosphatase, PTP zeta, is expressed in brain and has an N-terminal receptor domain homologous to carbonic anhydrases

<103> Proc. Natl. Acad. Sci. USA

<104> 89

<105> 16

<300>
 <301> Levy, J.B., et al.
 <302> The cloning of a receptor-type protein tyrosine phosphatase expressed
 in the central nervous system
 <303> J. Biol. Chem.
 <304> 268
 <305> 14
 <306> 10573-10581
 <307> 1993
 <309>
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Val Glu Glu Ile Gly Trp Ser Tyr Thr Gly Ala Leu Asn Gln Lys Asn
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Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile
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Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Lys Leu
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Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
 85 90 95

Asn Thr Gly Lys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
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Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
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His Trp Gly Lys Cys Asn Met Ser Ser Asp Gly Ser Glu His Ser Leu
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Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
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Phe Lys Ala Ile Ile Asp Gly Val Glu Ser Val Ser Arg Phe Gly Lys
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225 230 235 240

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Glu Ser Gln Leu Ala Val Phe Cys Glu Val Leu Thr Met Gln Gln Ser
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Gly Tyr Val Met Leu Met Asp Tyr Leu Gln Asn Asn Phe Arg Glu Gln
275 280 285

Gln Tyr Lys Phe Ser Arg Gln Val Phe Ser Ser Tyr Thr Gly Lys Glu
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Glu Ile His Glu Ala Val Cys Ser Ser Glu Pro Glu Asn Val Gln Ala
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Asp Pro Glu Asn Tyr Thr Ser Leu Leu Val Thr Trp Glu Arg Pro Arg
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Val Val Tyr Asp Thr Met Ile Glu Lys Phe Ala Val Leu Tyr Gln Gln
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Leu Asp Gly Glu Asp Gln Thr Lys His Glu Phe Leu Thr Asp Gly Tyr
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Gln Asp Leu Gly Ala Ile Leu Asn Asn Leu Leu Pro Asn Met Ser Tyr

Ser Asp Gln Leu Ile Val Asp Met Pro Thr Asp Asn Pro Glu Leu Asp
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Glu Gly Lys Asp Ile Glu Glu Gly Ala Ile Val Asn Pro Gly Arg Asp
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Ser Ala Thr Asn Gln Ile Arg Lys Lys Glu Pro Gln Ile Ser Thr Thr
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Thr His Tyr Asn Arg Ile Gly Thr Lys Tyr Asn Glu Ala Lys Thr Asn
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Arg Ser Pro Thr Arg Gly Ser Glu Phe Ser Gly Lys Gly Asp Val Pro
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Glu Lys Asp Ile Ser Leu Thr Ser Gln Thr Val Thr Glu Leu Pro Pro
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675 680 685

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Val Thr Asp Leu Glu Met Pro His Tyr Ser Thr Phe Ala Tyr Phe Pro
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725 730 735

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740 745 750

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755 760 765

Pro Leu Val Thr Pro Leu Leu Leu Asp Asn Gln Ile Leu Asn Thr Thr
770 775 780

Pro Ala Ala Ser Ser Ser Asp Ser Ala Leu His Ala Thr Pro Val Phe
785 790 795 800

Pro Ser Val Asp Val Ser Phe Glu Ser Ile Leu Ser Ser Tyr Asp Gly
805 810 815

Ala Pro Leu Leu Pro Phe Ser Ser Ala Ser Phe Ser Ser Glu Leu Phe
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850

855

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900 905 910

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Ala Leu Ser Asp Asn Glu Gly Ser Gln His Ile Phe Thr Val Ser Tyr
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Asp Gly Glu Trp Ser Gly Ala Ser Ser Asp Ser Glu Phe Leu Leu Pro
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<301> Kim, I., Moon, S.O., Koh, K.N., Kim, H., Uhm, C.S., Kwak, H.J., Kim, N.G. and Koh, G.Y.

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<303> J. Biol. Chem.

<304> 274

<305> 37

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<307> 1999

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Gln Ser Glu Ile Ile Ala Gln Leu Glu Glu His Cys Gln Arg Val Pro
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Tyr Gln Pro Pro Thr Tyr Asn Arg Ile Ile Asn Gln Ile Ser Thr Asn
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Glu Ile Gln Ser Asp Gln Asn Leu Lys Val Leu Pro Pro Pro Leu Pro
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Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys Pro Ser
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Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr Val Ile Gln
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Lys Ala Gly Ile Gly Asn Ile Arg Gly Ala Tyr Trp Ile Gly Leu Arg

340

345

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Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His
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Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu
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Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp
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Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
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Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
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Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr
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Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln
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Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala
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Gly Asp His Pro Val Glu Leu Leu Ala Arg Asp Phe Glu Lys Asn Tyr
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Asn Met Tyr Ile Phe Pro Val His Trp Gln Phe Gly Gln Leu Asp Gln
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His Pro Ile Asp Gly Tyr Leu Ser His Thr Glu Leu Ala Pro Leu Arg
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Ala Pro Leu Ile Pro Met Glu His Cys Thr Thr Arg Phe Phe Glu Thr
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 <301> Park,M., Dean,M., Kaul,K., Braun,M.J., Gonda,M.A. and Vande Woude,G.
 <302> Sequence of MET protooncogene cDNA has features characteristic of the
 tyrosine kinase family of growth-factor receptors
 <303> Proc. Natl. Acad. Sci. U.S.A.
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 Asn Phe Thr Ala Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His
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 His Ile Phe Leu Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu
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 Asp Leu Gln Lys Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His
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Tyr	Tyr	Asp	Asp	Gln	Leu	Ile	Ser	Cys	Gly	Ser	Val	Asn	Arg	Gly	Thr		
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Cys	Gln	Arg	His	Val	Phe	Pro	His	Asn	His	Thr	Ala	Asp	Ile	Gln	Ser		
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gag	gtt	cac	tgc	ata	ttc	tcc	cca	cag	ata	gaa	gag	ccc	agc	cag	tgt	710	
Glu	Val	His	Cys	Ile	Phe	Ser	Pro	Gln	Ile	Glu	Glu	Pro	Ser	Gln	Cys		
			160					165				170					
cct	gac	tgt	gtg	gtg	agc	gcc	ctg	gga	gcc	aaa	gtc	ctt	tca	tct	gta	758	
Pro	Asp	Cys	Val	Val	Ser	Ala	Leu	Gly	Ala	Lys	Val	Leu	Ser	Ser	Val		
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Lys	Asp	Arg	Phe	Ile	Asn	Phe	Phe	Val	Gly	Asn	Thr	Ile	Asn	Ser	Ser		
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Tyr	Phe	Pro	Asp	His	Pro	Leu	His	Ser	Ile	Ser	Val	Arg	Arg	Leu	Lys		
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Phe	Glu	Ser	Asn	Asn	Phe	Ile	Tyr	Phe	Leu	Thr	Val	Gln	Arg	Glu	Thr		
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Asn	Ser	Gly	Leu	His	Ser	Tyr	Met	Glu	Met	Pro	Leu	Glu	Cys	Ile	Leu		
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Phe Pro Ile Lys Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys			
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aac aat gtg aga tgt ctc cag cat ttt tac gga ccc aat cat gag cac			1382
Asn Asn Val Arg Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His			
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Cys Phe Asn Arg Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg			
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Arg Asp Glu Tyr Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp			
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Leu Phe Met Gly Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr			
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Phe Ile Lys Gly Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly			
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Arg Phe Met Gln Val Val Ser Arg Ser Gly Pro Ser Thr Pro His			
465	470	475	
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Val Asn Phe Leu Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val			
480	485	490	
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Glu His Thr Leu Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys			
495	500	505	
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Lys Ile Thr Lys Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln			
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Ser Cys Ser Gln Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp			
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cca acc aaa tct ttt att agt ggt ggg agt aca ata aca ggt gtt ggg Pro Thr Lys Ser Phe Ile Ser Gly Gly Ser Thr Ile Thr Gly Val Gly 750 755 760	2486
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Glu Lys Pro Val Met Ile Ser Met Gly Asn Glu Asn Val Leu Glu Ile	
845 850 855 860	
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Val Gly Asn Lys Ser Cys Glu Asn Ile His Leu His Ser Glu Ala Val	
880 885 890	
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Leu Cys Thr Val Pro Asn Asp Leu Leu Lys Leu Asn Ser Glu Leu Asn	
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910 915 920	
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Val Gln Pro Asp Gln Asn Phe Thr Gly Leu Ile Ala Gly Val Val Ser	
925 930 935 940	
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Ala Arg Val His Thr Pro His Leu Asp Arg Leu Val Ser Ala Arg Ser	
975 980 985	
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Val Ser Pro Thr Thr Glu Met Val Ser Asn Glu Ser Val Asp Tyr Arg	
990 995 1000	

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Leu	Thr	Ser	Gly	Asp	Ser	Asp	Ile	Ser	Ser	Pro	Leu	Leu	Gln	Asn		
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Thr	Val	His	Ile	Asp	Leu	Ser	Ala	Leu	Asn	Pro	Glu	Leu	Val	Gln		
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Phe	Asn	Glu	Val	Ile	Gly	Arg	Gly	His	Phe	Gly	Cys	Val	Tyr	His		
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Gly	Thr	Leu	Leu	Asp	Asn	Asp	Gly	Lys	Lys	Ile	His	Cys	Ala	Val		
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Lys	Ser	Leu	Asn	Arg	Ile	Thr	Asp	Ile	Gly	Glu	Val	Ser	Gln	Phe		
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Leu	Ser	Leu	Leu	Gly	Ile	Cys	Leu	Arg	Ser	Glu	Gly	Ser	Pro	Leu		
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Val	Val	Leu	Pro	Tyr	Met	Lys	His	Gly	Asp	Leu	Arg	Asn	Phe	Ile		
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Arg	Asn	Glu	Thr	His	Asn	Pro	Thr	Val	Lys	Asp	Leu	Ile	Gly	Phe		
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Gly	Leu	Gln	Val	Ala	Lys	Gly	Met	Lys	Tyr	Leu	Ala	Ser	Lys	Lys		
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Phe	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Asp	Glu		
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Tyr Arg Lys Thr Tyr Tyr Ala Val His Asn Lys Thr Gly Ala Lys

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Leu Pro Val Lys Trp Met Ala Leu Glu Ser	Leu Gln Thr Gln Lys		
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Glu Leu Met Thr Arg Gly Ala Pro Pro Tyr Pro	Asp Val Asn Thr		
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Phe Asp Ile Thr Val Tyr Leu Leu Gln Gly Arg	Arg Leu Leu Gln		
1290	1295	1300	
ccc gaa tac tgc cca gac ccc tta tat gaa gta	atg cta aaa tgc	4151	
Pro Glu Tyr Cys Pro Asp Pro Leu Tyr Glu Val	Met Leu Lys Cys		
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tgg cac cct aaa gcc gaa atg cgc cca tcc ttt	tct gaa ctg gtg	4196	
Trp His Pro Lys Ala Glu Met Arg Pro Ser Phe	Ser Glu Leu Val		
1320	1325	1330	
tcc cgg ata tca gcg atc ttc tct act ttc att	ggg gag cac tat	4241	
Ser Arg Ile Ser Ala Ile Phe Ser Thr Phe Ile	Gly Glu His Tyr		
1335	1340	1345	
gtc cat gtg aac gct act tat gtg aac gta aaa	tgt gtc gct ccg	4286	
Val His Val Asn Ala Thr Tyr Val Asn Val Lys	Cys Val Ala Pro		
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tat cct tct ctg ttg tca tca gaa gat aac gct	gat gat gag gtg	4331	
Tyr Pro Ser Leu Leu Ser Ser Glu Asp Asn Ala	Asp Asp Glu Val		
1365	1370	1375	
gac aca cga cca gcc tcc ttc tgg gag aca tca	tag tgctagtact	4377	
Asp Thr Arg Pro Ala Ser Phe Trp Glu Thr Ser			
1380	1385	1390	
atgtcaaaagc aacagtcac acccttgcca atgggttttt	cactgcccga cctttaaaag	4437	
gcacatcgata ttctttgtct cttgcacaaat tgcactatta	ataggacttg tattgttatt	4497	
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... .. 1. 4 .. 1. 4

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Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
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35 40 45

Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
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Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
65 70 75 80

Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
85 90 95

Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
100 105 110

Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr Tyr Tyr Asp Asp
115 120 125

Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
130 135 140

Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
145 150 155 160

Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
195 200 205

His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp
210 215 220

Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
225 230 235 240

Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
245 250 255

Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
260 265 270

Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
275 280 285

His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
290 295 300

Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala
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Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
325 330 335

Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
340 345 350

Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
355 360 365

Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
370 375 380

Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg

Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
420 425 430

Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
435 440 445

Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
450 455 460

Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
465 470 475 480

Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
485 490 495

Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys
500 505 510

Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln Ser Cys Ser Gln
515 520 525

Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
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Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
545 550 555 560

Cys Leu Pro Ala Ile Tyr Lys Val Phe Pro Asn Ser Ala Pro Leu Glu
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Gly Gly Thr Arg Leu Thr Ile Tyr Gly Thr Asp Phe Gly Ile Arg Arg
580 585 590

Asn Asn Lys Phe Asp Leu Lys Lys Thr Arg Val Leu Leu Gly Asn Glu
595 600 605

Ser Cys Thr Leu Thr Leu Ser Thr Ser Thr Met Asn Thr Leu Lys Tyr
610 615 620

865

870

875

880

Ser Cys Glu Asn Ile His Leu His Ser Glu Ala Val Leu Cys Thr Val
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Pro Asn Asp Leu Leu Lys Leu Asn Ser Glu Leu Asn Ile Glu Trp Lys
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Gln Ala Ile Ser Ser Thr Val Leu Gly Lys Val Ile Val Gln Pro Asp
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Gln Asn Phe Thr Gly Leu Ile Ala Gly Val Val Ser Ile Ser Thr Ala
 930 935 940

Leu Leu Leu Leu Leu Gly Phe Phe Leu Trp Leu Lys Lys Arg Lys Gln
 945 950 955 960

Ile Lys Asp Leu Gly Ser Glu Leu Val Arg Tyr Asp Ala Arg Val His
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Thr Pro His Leu Asp Arg Leu Val Ser Ala Arg Ser Val Ser Pro Thr
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Glu Asp Gln Phe Pro Asn Ser Ser Gln Asn Gly Ser Cys Arg Gln
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Val Gln Tyr Pro Leu Thr Asp Met Ser Pro Ile Leu Thr Ser Gly
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Asp Ser Asp Ile Ser Ser Pro Leu Leu Gln Asn Thr Val His Ile
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Ile Gly Arg Gly His Ile Gly Tyr Val Tyr His Gly Thr Leu Leu

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Arg	Ile	Thr	Asp	Ile	Gly	Glu	Val	Ser	Gln	Phe	Leu	Thr	Glu	Gly
	1115					1120					1125			
Ile	Ile	Met	Lys	Asp	Phe	Ser	His	Pro	Asn	Val	Leu	Ser	Leu	Leu
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Gly	Ile	Cys	Leu	Arg	Ser	Glu	Gly	Ser	Pro	Leu	Val	Val	Leu	Pro
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Tyr	Met	Lys	His	Gly	Asp	Leu	Arg	Asn	Phe	Ile	Arg	Asn	Glu	Thr
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His	Asn	Pro	Thr	Val	Lys	Asp	Leu	Ile	Gly	Phe	Gly	Leu	Gln	Val
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Ala	Lys	Gly	Met	Lys	Tyr	Leu	Ala	Ser	Lys	Lys	Phe	Val	His	Arg
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Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Asp	Glu	Lys	Phe	Thr	Val
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Lys	Val	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Met	Tyr	Asp	Lys	Glu
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Tyr	Tyr	Ser	Val	His	Asn	Lys	Thr	Gly	Ala	Lys	Leu	Pro	Val	Lys
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Trp	Met	Ala	Leu	Glu	Ser	Leu	Gln	Thr	Gln	Lys	Phe	Thr	Thr	Lys
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Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Val	Leu	Trp	Glu	Leu	Met	Thr
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Pro Asp Pro Leu Tyr Glu Val Met Leu Lys Cys Trp His Pro Lys
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Ala Glu Met Arg Pro Ser Phe Ser Glu Leu Val Ser Arg Ile Ser
1325 1330 1335

Ala Ile Phe Ser Thr Phe Ile Gly Glu His Tyr Val His Val Asn
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Ala Thr Tyr Val Asn Val Lys Cys Val Ala Pro Tyr Pro Ser Leu
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<301> Gary,S.C., Zerillo,C.A., Chiang,V.L., Gaw,J.U., Gray,G. and
Hockfield,S.

<302> cDNA cloning, chromosomal localization, and expression analysis of
human BEHAB/brevican, a brain specific proteoglycan regulated during cortical
development and in glioma

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Leu Phe Leu Pro Leu Leu Ala Ala Leu Val Leu Ala Gln Ala Pro Ala	
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gct tta gca gat gtt ctg gaa gga gac agc tca gag gac cgc gct ttt	152
Ala Leu Ala Asp Val Leu Glu Gly Asp Ser Ser Glu Asp Arg Ala Phe	
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Arg Val Arg Ile Ala Gly Asp Ala Pro Leu Gln Gly Val Leu Gly Gly	
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gcc ctc acc atc cct tgc cac gtc cac tac ctg cgg cca ccg ccg agc	248
Ala Leu Thr Ile Pro Cys His Val His Tyr Leu Arg Pro Pro Pro Ser	
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cgc cgg gct gtg ctg ggc tct ccg cgg gtc aag tgg act ttc ctg tcc	296
Arg Arg Ala Val Leu Gly Ser Pro Arg Val Lys Trp Thr Phe Leu Ser	
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Arg Gly Arg Glu Ala Glu Val Leu Val Ala Arg Gly Val Arg Val Lys	
85 90 95	
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Val Asn Glu Ala Tyr Arg Phe Arg Val Ala Leu Pro Ala Tyr Pro Ala	
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tgc ctc acc gac gtc tcc ctg gcg ctg agc gag ctg cgc ccc aac gac	440
Ser Leu Thr Asp Val Ser Leu Ala Leu Ser Glu Leu Arg Pro Asn Asp	
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tca ggt atc tat cgc tgt gag gtc cag cac ggc atc gat gac agc agc	488
Ser Gly Ile Tyr Arg Cys Glu Val Gln His Gly Ile Asp Asp Ser Ser	
135 140 145	
gac gct gtg gag gtc aag gtc aaa ggg gtc gtc ttt ctc tac cga gag	536
Asp Ala Val Glu Val Lys Val Lys Gly Val Val Phe Leu Tyr Arg Glu	
150 155 160	
ggc tct gcc cgc tat gct ttc tcc ttt tct ggg gcc cag gag gcc tgt	584
Gly Ser Ala Arg Tyr Ala Phe Ser Phe Ser Gly Ala Gln Glu Ala Cys	
165 170 175	
gcc cgc att gga gcc cac atc gcc acc ccg gag cag ctc tat gcc gcc	632
Ala Arg Ile Gly Ala His Ile Ala Thr Pro Glu Gln Leu Tyr Ala Ala	

acc gtg agg tat ccc atc cag acc cca cga gag gcc tgt tac gga gac	728
Thr Val Arg Tyr Pro Ile Gln Thr Pro Arg Glu Ala Cys Tyr Gly Asp	
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Met Asp Gly Phe Pro Gly Val Arg Asn Tyr Gly Val Val Asp Pro Asp	
230 235 240	
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245 250 255	
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Phe Leu Gly Asp Pro Pro Glu Lys Leu Thr Leu Glu Glu Ala Arg Ala	
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Tyr Cys Gln Glu Arg Gly Ala Glu Ile Ala Thr Thr Gly Gln Leu Tyr	
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Ala Ala Trp Asp Gly Gly Leu Asp His Cys Ser Pro Gly Trp Leu Ala	
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Asp Gly Ser Val Arg Tyr Pro Ile Val Thr Pro Ser Gln Arg Cys Gly	
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Gly Gly Leu Pro Gly Val Lys Thr Leu Phe Leu Phe Pro Asn Gln Thr	
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360 365 370	
cca gcc tct gat gga cta gag gct atc gtc aca gtg aca gag acc ctg	1208
Pro Ala Ser Asp Gly Leu Glu Ala Ile Val Thr Val Thr Glu Thr Leu	
375 380 385	
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Glu Glu Leu Gln Leu Pro Gln Glu Ala Thr Glu Ser Glu Ser Arg Gly	
390 395 400	
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Ala Ile Tyr Ser Ile Pro Ile Met Glu Asp Gly Gly Gly Gly Ser Ser	
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gca	ttg	gag	gaa	gaa	gag	aaa	tat	gaa	gat	gaa	gaa	gag	aaa	gag	gag	1448
Ala	Leu	Glu	Glu	Glu	Glu	Lys	Tyr	Glu	Asp	Glu	Glu	Glu	Lys	Glu	Glu	
			455					460					465			
gaa	gaa	gaa	gag	gag	gag	gtg	gag	gat	gag	gct	ctg	tgg	gca	tgg	ccc	1496
Glu	Glu	Glu	Glu	Glu	Glu	Val	Glu	Asp	Glu	Ala	Leu	Trp	Ala	Trp	Pro	
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Ser	Glu	Leu	Ser	Ser	Pro	Gly	Pro	Glu	Ala	Ser	Leu	Pro	Thr	Glu	Pro	
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Ala	Ala	Gln	Glu	Glu	Ser	Leu	Ser	Gln	Ala	Pro	Ala	Arg	Ala	Val	Leu	
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Gln	Pro	Gly	Ala	Ser	Pro	Leu	Pro	Asp	Gly	Glu	Ser	Glu	Ala	Ser	Arg	
			520						525				530			
cct	cca	agg	gtc	cat	gga	cca	cct	act	gag	act	ctg	ccc	act	ccc	agg	1688
Pro	Pro	Arg	Val	His	Gly	Pro	Pro	Thr	Glu	Thr	Leu	Pro	Thr	Pro	Arg	
			535					540					545			
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Glu	Arg	Asn	Leu	Ala	Ser	Pro	Ser	Pro	Ser	Thr	Leu	Val	Glu	Ala	Arg	
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gag	gtg	ggg	gag	gca	act	ggt	ggt	cct	gag	cta	tct	ggg	gtc	cct	cga	1784
Glu	Val	Gly	Glu	Ala	Thr	Gly	Gly	Pro	Glu	Leu	Ser	Gly	Val	Pro	Arg	
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gga	gag	agc	gag	gag	aca	gga	agc	tcc	gag	ggt	gcc	cct	tcc	ctg	ctt	1832
Gly	Glu	Ser	Glu	Glu	Thr	Gly	Ser	Ser	Glu	Gly	Ala	Pro	Ser	Leu	Leu	
580					585				590					595		
cca	gcc	aca	cgg	gcc	cct	gag	ggt	acc	agg	gag	ctg	gag	gcc	ccc	tct	1880
Pro	Ala	Thr	Arg	Ala	Pro	Glu	Gly	Thr	Arg	Glu	Leu	Glu	Ala	Pro	Ser	
			600					605					610			
gaa	gat	aat	tct	gga	aga	act	gcc	cca	gca	ggg	acc	tca	gtg	cag	gcc	1928
Glu	Asp	Asn	Ser	Gly	Arg	Thr	Ala	Pro	Ala	Gly	Thr	Ser	Val	Gln	Ala	
			615				620					625				
cag	cca	gtg	ctg	ccc	act	gac	agc	gcc	agc	cga	ggt	gga	gtg	gcc	gtg	1976
Gln	Pro	Val	Leu	Pro	Thr	Asp	Ser	Ala	Ser	Arg	Gly	Gly	Val	Ala	Val	
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Leu Leu Leu Phe Phe Phe Leu Gln Leu Thr Val Thr

660

665

670

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Ala Pro Ala Ala Leu Ala Asp Val Leu Glu Gly Asp Ser Ser Glu Asp
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Arg Ala Phe Arg Val Arg Ile Ala Gly Asp Ala Pro Leu Gln Gly Val
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Leu Gly Gly Ala Leu Thr Ile Pro Cys His Val His Tyr Leu Arg Pro
50           55           60

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Pro Pro Ser Arg Arg Ala Val Leu Gly Ser Pro Arg Val Lys Trp Thr

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Arg Val Lys Val Asn Glu Ala Tyr Arg Phe Arg Val Ala Leu Pro Ala
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Tyr Pro Ala Ser Leu Thr Asp Val Ser Leu Ala Leu Ser Glu Leu Arg
115 120 125

Pro Asn Asp Ser Gly Ile Tyr Arg Cys Glu Val Gln His Gly Ile Asp
130 135 140

Asp Ser Ser Asp Ala Val Glu Val Lys Val Lys Gly Val Val Phe Leu
145 150 155 160

Tyr Arg Glu Gly Ser Ala Arg Tyr Ala Phe Ser Phe Ser Gly Ala Gln
165 170 175

Glu Ala Cys Ala Arg Ile Gly Ala His Ile Ala Thr Pro Glu Gln Leu
180 185 190

Tyr Ala Ala Tyr Leu Gly Gly Tyr Glu Gln Cys Asp Ala Gly Trp Leu
195 200 205

Ser Asp Gln Thr Val Arg Tyr Pro Ile Gln Thr Pro Arg Glu Ala Cys
210 215 220

Tyr Gly Asp Met Asp Gly Phe Pro Gly Val Arg Asn Tyr Gly Val Val
225 230 235 240

Asp Pro Asp Asp Leu Tyr Asp Val Tyr Cys Tyr Ala Glu Asp Leu Asn
245 250 255

Gly Glu Leu Phe Leu Gly Asp Pro Pro Glu Lys Leu Thr Leu Glu Glu
260 265 270

Ala Arg Ala Tyr Cys Gln Glu Arg Gly Ala Glu Ile Ala Thr Thr Gly
275 280 285

Gln Leu Tyr Ala Ala Thr Asp Gly Gly Leu Asp His Cys Ser Pro Gly
290 295 300

545 550 555 560

Glu Ala Arg Glu Val Gly Glu Ala Thr Gly Gly Pro Glu Leu Ser Gly
565 570 575

Val Pro Arg Gly Glu Ser Glu Glu Thr Gly Ser Ser Glu Gly Ala Pro
580 585 590

Ser Leu Leu Pro Ala Thr Arg Ala Pro Glu Gly Thr Arg Glu Leu Glu
595 600 605

Ala Pro Ser Glu Asp Asn Ser Gly Arg Thr Ala Pro Ala Gly Thr Ser
610 615 620

Val Gln Ala Gln Pro Val Leu Pro Thr Asp Ser Ala Ser Arg Gly Gly
625 630 635 640

Val Ala Val Val Pro Ala Ser Gly Asn Ser Ala Gln Gly Ser Thr Ala
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Leu Ser Ile Leu Leu Leu Phe Phe Pro Leu Gln Leu Trp Val Thr
660 665 670

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<223> Human mRNA for CD44E (epithelial form)

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<222> (124)..(1605)
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<301> Stamenkovic,I., Aruffo,A., Amiot,M. and Seed,B.
<302> The hematopoietic and epithelial forms of CD44 are distinct
polypeptides with different adhesion potentials for hyaluronate-bearing cells
<303> EMBO J.

195	200	205	
gac agt ccc tgg atc acc gac agc aca gac aga atc cct cgt acc aat			792
Asp Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn			
210	215	220	
atg gac tcc agt cat agt aca acg ctt cag cct act gca aat cca aac			840
Met Asp Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn			
225	230	235	
aca ggt ttg gtg gaa gat ttg gac agg aca gga cct ctt tca atg aca			888
Thr Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr			
240	245	250	255
acg cag cag agt aat tct cag agc ttc tct aca tca cat gaa ggc ttg			936
Thr Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu			
260	265	270	
gaa gaa gat aaa gac cat cca aca act tct act ctg aca tca agc aat			984
Glu Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn			
275	280	285	
agg aat gat gtc aca ggt gga aga aga gac cca aat cat tct gaa ggc			1032
Arg Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly			
290	295	300	
tca act cat tta ctg gaa ggt tat acc tct cat tac cca cac acg aag			1080
Ser Thr His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys			
305	310	315	
gaa agc agg acc ttc atc cca gtg acc tca gct aag act ggg tcc ttt			1128
Glu Ser Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe			
320	325	330	335
gga gtt act gca gtt act gtt gga gat tcc aac tct aat gtc aat cgt			1176
Gly Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg			
340	345	350	
tcc tta tca gga gac caa gac aca ttc cac ccc agt ggg ggg tcc cat			1224
Ser Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His			
355	360	365	
acc act cat gga tct gaa tca gat gga cac tca cat ggg agt caa gaa			1272
Thr Thr His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu			
370	375	380	
ggg gga gca aac aca acc tct ggt cct ata agg aca ccc caa att cca			1320
Gly Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro			
385	390	395	
gaa tgg cta atc atc tta gaa tcc cta tta acc tta act tta att ctt			1368

aag cta gtg atc aac agt ggc aat gga gct gtg gag gac aga aag cca	1464
Lys Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro	
435 440 445	
agt gga ctc aac gga gag gcc agc aag tct cag gaa atg gtg cat ttg	1512
Ser Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu	
450 455 460	
gtg aac aag gag tgg tca gaa act cca gac cag ttt atg aca gct gat	1560
Val Asn Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp	
465 470 475	
gag aca agg aac ctg cag aat gtg gac atg aag att ggg gtg taa	1605
Glu Thr Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val	
480 485 490	
cacctacacc attatcttgg aaagaaacaa cgttggaac ataaccatta caggggagct	1665
gggacactta acagatgcaa tgtgctactg attgtttcat ttcgaaatcta taatagcata	1725
aaattttcta ctctttttgt tttttgtgtt ttgttcttta aagtcagggtc caatttgtaa	1785
aaacagcatt gottttctgaa attagggccc aattaataat cagcaagaat tttgatcggt	1845
tcagttcccc acttgagggc ctttcatccc tcgggtgtgc tatggatggc ttctaacaaa	1905
aacctaccac atagttatct ctgatcgcca accttgcccc ccaccagcta aggacatttc	1965
caggggttaat agggcctggc cctgggagga aatttgaatg ggtcattttg cccttcatt	2025
agcctaatec ctgggcattg ctttccactg aggttggggg ttgggggtgta ctagttacac	2085
atcttcaaca gacccctct agaaattttt cagatgcttc tgggagacac ccaaagggtg	2145
agtctattta tctgtagtaa actatttate tgtgtttttg aaatattaaa ccttgatca	2205
gtccttttat tcagtataat tttttaaagt tactttgtca gaggcacaaa aagggtttta	2265
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 <123> BY SIMILARITY

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 <223> CD44 ANTIGEN

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 <223> POTENTIAL

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 <223> LINK

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 <223> PYRROLIDONE CARBOXYLIC ACID (PROBABLE)

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 <222> (53)..(118)
 <223> BY SIMILARITY

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 <222> (77)..(97)
 <223> BY SIMILARITY

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<223> N-LINKED (GLCNAC ...) (POTENTIAL)

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<223> N-LINKED (GLCNAC ...) (POTENTIAL)

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<223> N-LINKED (GLCNAC ...) (POTENTIAL)

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<223> MISSING (IN ISOFORM CD44SP)

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<223> G -> A (IN ISOFORM WITH ALTERNATIVE SPLICE DONOR/ACCEPTOR ON EXON
      5)

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<222> (193)..(223)
<223> MISSING (IN ISOFORM WITH ALTERNATIVE SPLICE DONOR/ACCEPTOR ON EXO
      N 5)

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 <223> MISSING (IN ISOFORM WITHOUT EXON 6)

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 <223> T -> H (IN ISOFORMS WITHOUT EXONS 6 TO 11)

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 <223> MISSING (IN ISOFORMS WITHOUT EXONS 6 TO 11)

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 <223> T -> R (IN ISOFORMS WITHOUT EXONS 6 TO 14)

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 <223> MISSING (IN ISOFORM WITH ALTERNATIVE SPLICE DONOR/ACCEPTOR ON EXO
 N 7)

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 <223> I -> T (IN ISOFORMS WITHOUT EXON 10)

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 <222> (386)..(428)
 <223> MISSING (IN ISOFORMS WITHOUT EXON 10)

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 <223> Q -> R (IN ISOFORMS WITHOUT EXON 13)

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 <223> MISSING (IN ISOFORMS WITHOUT EXON 13)

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<223> MISSING (IN ISOFORMS WITHOUT EXON 14)

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<221> VARSPLIC

<222> (675)..(675)

<223> R -> S (IN ISOFORMS WITHOUT EXON 19)

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<221> VARSPLIC

<222> (676)..(742)

<223> MISSING (IN ISOFORMS WITHOUT EXON 19)

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<223> R -> P (IN IN(A) ANTIGEN)

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Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
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Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
20 25 30

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
35 40 45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
65 70 75 80

Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
85 90 95

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser
100 105 110

Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
115 120 125

Ile Thr Ile Val Asn Ala Arg Gly Thr Ala Tyr Val Glu Tyr Gly Ala

145 150 155 160

Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
165 170 175

Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
180 185 190

Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
195 200 205

Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Thr Leu
210 215 220

Met Ser Thr Ser Ala Thr Ala Thr Glu Thr Ala Thr Lys Arg Gln Glu
225 230 235 240

Thr Trp Asp Trp Phe Ser Trp Leu Phe Leu Pro Ser Glu Ser Lys Asn
245 250 255

His Leu His Thr Thr Thr Gln Met Ala Gly Thr Ser Ser Asn Thr Ile
260 265 270

Ser Ala Gly Trp Glu Pro Asn Glu Glu Asn Glu Asp Glu Arg Asp Arg
275 280 285

His Leu Ser Phe Ser Gly Ser Gly Ile Asp Asp Asp Glu Asp Phe Ile
290 295 300

Ser Ser Thr Ile Ser Thr Thr Pro Arg Ala Phe Asp His Thr Lys Gln
305 310 315 320

Asn Gln Asp Trp Thr Gln Trp Asn Pro Ser His Ser Asn Pro Glu Val
325 330 335

Leu Leu Gln Thr Thr Thr Arg Met Thr Asp Val Asp Arg Asn Gly Thr
340 345 350

Leu Leu Gln Thr Thr Thr Arg Met Thr Asp Val Asp Arg Asn Gly Thr
355 360 365 370 375 380 385 390 395 400

Ile Gln Ala Thr Pro Ser Ser Thr Thr Glu Glu Thr Ala Thr Gln Lys
385 390 395 400

Glu Gln Trp Phe Gly Asn Arg Trp His Glu Gly Tyr Arg Gln Thr Pro
405 410 415

Arg Glu Asp Ser His Ser Thr Thr Gly Thr Ala Ala Ala Ser Ala His
420 425 430

Thr Ser His Pro Met Gln Gly Arg Thr Thr Pro Ser Pro Glu Asp Ser
435 440 445

Ser Trp Thr Asp Phe Phe Asn Pro Ile Ser His Pro Met Gly Arg Gly
450 455 460

His Gln Ala Gly Arg Arg Met Asp Met Asp Ser Ser His Ser Thr Thr
465 470 475 480

Leu Gln Pro Thr Ala Asn Pro Asn Thr Gly Leu Val Glu Asp Leu Asp
485 490 495

Arg Thr Gly Pro Leu Ser Met Thr Thr Gln Gln Ser Asn Ser Gln Ser
500 505 510

Phe Ser Thr Ser His Glu Gly Leu Glu Glu Asp Lys Asp His Pro Thr
515 520 525

Thr Ser Thr Leu Thr Ser Ser Asn Arg Asn Asp Val Thr Gly Gly Arg
530 535 540

Arg Asp Pro Asn His Ser Glu Gly Ser Thr Thr Leu Leu Glu Gly Tyr
545 550 555 560

Thr Ser His Tyr Pro His Thr Lys Glu Ser Arg Thr Phe Ile Pro Val
565 570 575

Thr Ser Ala Lys Thr Gly Ser Phe Gly Val Thr Ala Val Thr Val Gly

Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser Glu Ser Asp
610 615 620

Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr Ser Gly
625 630 635 640

Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu Ala Ser
645 650 655

Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val Asn Ser
660 665 670

Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn Ser Gly Asn
675 680 685

Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu Ala Ser
690 695 700

Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser Glu Thr
705 710 715 720

Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln Asn Val
725 730 735

Asp Met Lys Ile Gly Val
740

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<222> (1)..(930)
<223> Tetraspan TM4SF (TSPAN-3), mRNA

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LOC101928
TSPAN-3 protein, human

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 atg ggc cag tgc ggc atc acc tcc tcc aag acc gtg ctg gtc ttt etc 48
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 1 5 10 15

aac ctc atc ttc tgg ggg gca gct ggc att tta tgc tat gtg gga gcc 96
 Asn Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala
 20 25 30

tat gtc ttc atc act tat gat gac tat gac cac ttc ttt gaa gat gtg 144
 Tyr Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val
 35 40 45

tac acg ctc atc cct gct gta gtg atc ata gct gta gga gcc ctg ctt 192
 Tyr Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Gly Ala Leu Leu
 50 55 60

ttc atc att ggg cta att ggc tgc tgt gcc aca atc cgg gaa agt cgc 240
 Phe Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg
 65 70 75 80

tgt gga ctt gcc acg ttt gtc atc atc ctg ctc ttg gtt ttt gtc aca 288
 Cys Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr
 85 90 95

gaa gtt gtt gta gtg gtt ttg gga tat gtt tac aga gca aag gtg gaa 336
 Glu Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu
 100 105 110

aat gag gtt gat cgc agc att cag aaa gtg tat aag acc tac aat gga 384
 Asn Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys Thr Tyr Asn Gly
 115 120 125

acc aac cct gat gct gct agc cgg gct att gat tat gta gag aga gag 432
 Thr Asn Pro Asp Ala Ala Ser Arg Ala Ile Asp Tyr Val Gln Arg Gln
 130 135 140

ctg cat tgt tgt gga att cac aac tac tca gac tgg gaa aat aca gat 480
 Leu His Cys Cys Gly Ile His Asn Tyr Ser Asp Trp Glu Asn Thr Asp
 145 150 155 160

tgg ttc aaa gaa acc aaa aac gag agt gtc cct ctt agc tgc tgc aga 528
 Trp Phe Lys Glu Thr Lys Asn Gln Ser Val Pro Leu Ser Cys Cys Arg

tat gct gag ggg tgt gag gct cta gtt gtg aag aag cta caa gaa atc	624
Tyr Ala Glu Gly Cys Glu Ala Leu Val Val Lys Lys Leu Gln Glu Ile	
195 200 205	
atg atg cat gtg atc tgg gcc gca ctg gca ttt gca gct att cag ctg	672
Met Met His Val Ile Trp Ala Ala Leu Ala Phe Ala Ala Ile Gln Leu	
210 215 220	
ctg gcc atg ctg tgt gct tgc atc gtg ttg tgc aga agg agt aga gat	720
Leu Gly Met Leu Cys Ala Cys Ile Val Leu Cys Arg Arg Ser Arg Asp	
225 230 235 240	
cct gct tac gag ctc ctc atc act gcc gga acc tat gca tag	762
Pro Ala Tyr Glu Leu Leu Ile Thr Gly Gly Thr Tyr Ala	
245 250	
ttgacaactc ttgcctgagc tttttggtct tgttctgatt tggaaggtga attgagcagg	822
tctgctgctg ttggcctctg gagttcattt agttaagca catgtacact ggtgttggac	882
agagcagctt ggcttttcat gtgcccaact acttactact actgcgat	930

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 <223> Potential

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 <223> Extracellular (Potential)

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 <222> (51)..(71)

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 <223> Potential

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 <223> Extracellular (potential)

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 <223> Potential

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 <223> Cytoplasmic (potential)

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 <223> N-linked (GLCNAC...) (potential)

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Asn Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala
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Tyr Thr Leu Ile Phe Ala Val Val Ile Ile Ala Val Gly Ala Leu Leu

50

55

60

Phe Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg
65 70 75 80

Cys Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr
85 90 95

Glu Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu
100 105 110

Asn Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys Thr Tyr Asn Gly
115 120 125

Thr Asn Pro Asp Ala Ala Ser Arg Ala Ile Asp Tyr Val Gln Arg Gln
130 135 140

Leu His Cys Cys Gly Ile His Asn Tyr Ser Asp Trp Glu Asn Thr Asp
145 150 155 160

Trp Phe Lys Glu Thr Lys Asn Gln Ser Val Pro Leu Ser Cys Cys Arg
165 170 175

Glu Thr Ala Ser Asn Cys Asn Gly Ser Leu Ala His Pro Ser Asp Leu
180 185 190

Tyr Ala Glu Gly Cys Glu Ala Leu Val Val Lys Lys Leu Gln Glu Ile
195 200 205

Met Met His Val Ile Trp Ala Ala Leu Ala Phe Ala Ala Ile Gln Leu
210 215 220

Leu Gly Met Leu Cys Ala Cys Ile Val Leu Cys Arg Arg Ser Arg Asp
225 230 235 240

Pro Ala Tyr Glu Leu Leu Ile Thr Gly Gly Thr Tyr Ala
245 250

Ile Tyr Thr Leu Gly Tyr Ser Val Ser Leu Met Ser Leu Ala Thr Gly	
130 135 140	
agc ata att ctg tgc ctc ttc agg aag ctg cac tgc acc agg aat tac	480
Ser Ile Ile Leu Cys Leu Phe Arg Lys Leu His Cys Thr Arg Asn Tyr	
145 150 155 160	
atc cac ctg aac ctg ttc ctg tcc ttc atc ctg aga gcc atc tca gtg	528
Ile His Leu Asn Leu Phe Leu Ser Phe Ile Leu Arg Ala Ile Ser Val	
165 170 175	
ctg gtc aag gac gac gtt ctc tac tcc agc tct ggc acg ttg cac tgc	576
Leu Val Lys Asp Asp Val Leu Tyr Ser Ser Ser Gly Thr Leu His Cys	
180 185 190	
cct gac cag cca tcc tcc tgg gtg ggc tgc aag ctg agc ctg gtc ttc	624
Pro Asp Gln Pro Ser Ser Trp Val Gly Cys Lys Leu Ser Leu Val Phe	
195 200 205	
ctg cag tac tgc atc atg gcc aac ttc ttc tgg ctg ctg gtg gag ggg	672
Leu Gln Tyr Cys Ile Met Ala Asn Phe Phe Trp Leu Leu Val Glu Gly	
210 215 220	
ctc tac ctc cac acc ctc ctg gtg gcc atg ctc ccc cct aga agg tgc	720
Leu Tyr Leu His Thr Leu Leu Val Ala Met Leu Pro Pro Arg Arg Cys	
225 230 235 240	
ttc ctg gcc tac ctc ctg atc gga tgg ggc ctc ccc acc gtc tgc atc	768
Phe Leu Ala Tyr Leu Leu Ile Gly Trp Gly Leu Pro Thr Val Cys Ile	
245 250 255	
ggg gca tgg act gcg gcc agg ctc tac tta gaa gac acc ggt tgc tgg	816
Gly Ala Trp Thr Ala Ala Arg Leu Tyr Leu Glu Asp Thr Gly Cys Trp	
260 265 270	
gat aca aac gac cac agt gtg ccc tgg tgg gtc ata cga ata ccg att	864
Asp Thr Asn Asp His Ser Val Pro Trp Trp Val Ile Arg Ile Pro Ile	
275 280 285	
tta att tcc atc atc gtc aat ttc gtc ctt ttc att agt att ata cga	912
Leu Ile Ser Ile Ile Val Asn Phe Val Leu Phe Ile Ser Ile Ile Arg	
290 295 300	
att ttg ctg cag aag tta asa tcc cca gat gtc ggc ggc aac gac cag	960
Ile Leu Leu Gln Lys Leu Thr Ser Pro Asp Val Gly Gly Asn Asp Gln	
305 310 315 320	
tct cag tac aag agg ctg gcc aag tcc acg ctc ctg ctt atc ccg ctg	1008
Ser Gln Tyr Lys Arg Leu Ala Lys Ser Thr Leu Leu Leu Ile Pro Leu	
325 330 335	

Ser Lys Tyr Gln Ile Leu Phe Val Leu Tyr Leu Gly Ser Phe Gln Gly

355	360	365	
ctg gtg gtg gcc gtc ctc tac tgt ttc ctg aac agt gag gtg cag tgc			1152
Leu Val Val Ala Val Leu Tyr Cys Phe Leu Asn Ser Glu Val Gln Cys			
370	375	380	
gag ctg aag cga aaa tgg cga agc cgg tgc ccg acc ccg tcc gcg agc			1200
Glu Leu Lys Arg Lys Trp Arg Ser Arg Cys Pro Thr Pro Ser Ala Ser			
385	390	395	400
ccg gat tac agg gtc tgc ggt tcc tcc ttc tcc cac aac ggc tcg gag			1248
Arg Asp Tyr Arg Val Cys Gly Ser Ser Phe Ser His Asn Gly Ser Glu			
405	410	415	
ggc gcc ctg cag ttc cac cgc gcg tcc cga gcc cag tcc ttc ctg caa			1296
Gly Ala Leu Gln Phe His Arg Ala Ser Arg Ala Gln Ser Phe Leu Gln			
420	425	430	
acg gag acc tcg gtc atc tag			1317
Thr Glu Thr Ser Val Ile			
435			

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<223> 2 (Potential)

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<221> DOMAIN
<222> (179)..(203)
<223> Extracellular (Potential)

<220>
<221> TRANSMEM
<222> (204)..(227)
<223> 3 (Potential)

<220>
<221> DOMAIN
<222> (228)..(240)
<223> Cytoplasmic (Potential)

<220>
<221> TRANSMEM
<222> (241)..(262)
<223> 4 (Potential)

<220>
<221> DOMAIN
<222> (263)..(279)
<223> Extracellular (Potential)

<220>
<221> TRANSMEM
<222> (280)..(303)
<223> 5 (Potential)

<220>
<221> DOMAIN
<222> (304)..(328)
<223> Cytoplasmic (Potential)

<220>
<221> TRANSMEM
<222> (329)..(348)
<223> 6 (Potential)

<220>
<221> DOMAIN
<222> (349)..(360)
<223> Extracellular (Potential)

<224>

<221> DOMAIN
<222> (381)..(438)
<223> Cytoplasmic (potential)

<220>
<221> CARBOHYD
<222> (58)..(58)
<223> N-linked (GLCNAC...) (Potential)

<220>
<221> CARBOHYD
<222> (88)..(88)
<223> N-linked (GLCNAC...) (Potential)

<220>
<221> CARBOHYD
<222> (92)..(92)
<223> N-linked (GLCNAC...) (Potential)

<400> 20

Met Arg Thr Leu Leu Pro Pro Ala Leu Leu Thr Cys Trp Leu Leu Ala
1 5 10 15

Pro Val Asn Ser Ile His Pro Glu Cys Arg Phe His Leu Glu Ile Gln
20 25 30

Glu Glu Glu Thr Lys Cys Ala Glu Leu Leu Arg Ser Gln Thr Glu Lys
35 40 45

His Lys Ala Cys Ser Gly Val Trp Asp Asn Ile Thr Cys Trp Arg Pro
50 55 60

Ala Asn Val Gly Glu Thr Val Thr Val Pro Cys Pro Lys Val Phe Ser
65 70 75 80

Asn Phe Tyr Ser Lys Ala Gly Asn Ile Ser Lys Asn Cys Thr Ser Asp
85 90 95

Gly Trp Ser Glu Thr Phe Pro Asp Phe Val Asp Ala Cys Gly Tyr Ser
100 105 110

Asp Pro Glu Asp Glu Ser Lys Ile Thr Phe Tyr Ile Leu Val Lys Ala

Ser Ile Ile Leu Cys Leu Phe Arg Lys Leu His Cys Thr Arg Asn Tyr
145 150 155 160

Ile His Leu Asn Leu Phe Leu Ser Phe Ile Leu Arg Ala Ile Ser Val
165 170 175

Leu Val Lys Asp Asp Val Leu Tyr Ser Ser Ser Gly Thr Leu His Cys
180 185 190

Pro Asp Gln Pro Ser Ser Trp Val Gly Cys Lys Leu Ser Leu Val Phe
195 200 205

Leu Gln Tyr Cys Ile Met Ala Asn Phe Phe Trp Leu Leu Val Glu Gly
210 215 220

Leu Tyr Leu His Thr Leu Leu Val Ala Met Leu Pro Pro Arg Arg Cys
225 230 235 240

Phe Leu Ala Tyr Leu Leu Ile Gly Trp Gly Leu Pro Thr Val Cys Ile
245 250 255

Gly Ala Trp Thr Ala Ala Arg Leu Tyr Leu Glu Asp Thr Gly Cys Trp
260 265 270

Asp Thr Asn Asp His Ser Val Pro Trp Trp Val Ile Arg Ile Pro Ile
275 280 285

Leu Ile Ser Ile Ile Val Asn Phe Val Leu Phe Ile Ser Ile Ile Arg
290 295 300

Ile Leu Leu Gln Lys Leu Thr Ser Pro Asp Val Gly Gly Asn Asp Gln
305 310 315 320

Ser Gln Tyr Lys Arg Leu Ala Lys Ser Thr Leu Leu Leu Ile Pro Leu
325 330 335

Phe Gly Val His Tyr Met Val Phe Ala Val Phe Pro Ile Ser Ile Ser
340 345 350

<220>
 <221> SIGNAL
 <222> (1)..(32)
 <223>

<220>
 <221> GENE
 <222> (1)..(168)
 <223> Pleiotrophin

<220>
 <221> CHAIN
 <222> (33)..(168)
 <223> Pleiotrophin

<220>
 <221> DISULFID
 <222> (47)..(76)
 <223> By similarity.

<220>
 <221> DISULFID
 <222> (55)..(85)
 <223> By similarity.

<220>
 <221> DISULFID
 <222> (62)..(89)
 <223> By similarity.

<220>
 <221> DISULFID
 <222> (99)..(131)
 <223> By similarity.

<220>
 <221> DISULFID
 <222> (109)..(141)
 <223> By similarity.

<400> 22

Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala
 1 5 10 15

Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala
 20 25 30

Gln Arg Gln Arg Gln Val Tyr Val Gln Ile Phe Gly Arg Tyr Gly Phe

50

55

60

Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met
65 70 75 80

Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly
85 90 95

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
100 105 110

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn
115 120 125

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu
130 135 140

Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys Lys Glu Gly
145 150 155 160

Lys Lys Gln Glu Lys Met Leu Asp
165

<210> 23
<211> 3143
<212> DNA
<213> Homo sapiens

<220>
<221> Gene
<222> (1)..(3143)
<223> Osteopontin

<220>
<221> CDS
<222> (374)..(427)
<223>

<220>
<221> CDS
<222> (537)..(575)
<223>

Lys Gln
30

cgagaggtgc aagaaacgta ttgctgcga tcaaagaggt tcatatttgt aaagcaattt 685

gaaagagtgct ctagccacaca gtaagtgcga cataagaggt tgttaaatga atctgcaaaa 745

aaaaaaaaaa ttacaaaaag gtacctaagg gtccgggtga ctatatgctt ccatcaagac 805

tagtgaagaa tgggtgtttt ttccattcat ccctacattt ctttttttaa taatgataaa 865

catgcaactt tttttagt ctt tac aac aaa tac cca gat gct gtg gcc aca 916
Leu Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr
35 40

tgg cta aac cct gac cca tct cag aag cag aat ctc cta gcc cca cag 964
Trp Leu Asn Pro Asp Pro Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln
45 50 55

gtatttttaa acttttcata attaaactac agtgatgaaa gatagccaca ctcaggccat 1024

ttgggtgct cagatgaatc ctgcctgcc tgctggcaaa catgtgctta ggacattgac 1084

tgatctgcca tgttggttct tctctgtgtt aagccatcca cagatgaggc tgaaaaataa 1144

aaactgcttt ggattaaaaa ggttaacttt tgaataaaaa agctaggcat gtgtgatgcy 1204

cactaacag tgccattcct tcttcag aat gct gtg tcc tct gaa gaa acc aat 1258
Asn Ala Val Ser Ser Glu Glu Thr Asn
60 65

gac ttt aaa caa gag gtaagttctc attttcaatc agaggcccat catgccttga 1313
Asp Phe Lys Gln Glu
70

agagatgaaa gaaggcattg cctggattct cttctgatga aatttcatta gcaagttttc 1373

cagctaattg gcagtctaaa acttgctcat aaataaaaca tgtatttact aaatatcaga 1433

aatactaggt ttctcggat aacctaaaag ccatgggatg tactgtgaat gcaaagattc 1493

tgaaactaaa taaaaagaaa gatagtaaaa gactaatgtg ctataaaggc taagggaaaa 1553

taaaaaccca tatattaatt ttccggcca tcttaatttt cag acc ctt cca agt 1608
Thr Leu Pro Ser
75

aag tcc aac gaa agc cat gac cac atg gat gat atg gat gat gaa gat 1656
Lys Ser Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp
80 85 90

Arg Arg Thr Arg Arg Thr Arg Arg Pro His Ala Ser Arg Glu Ser His

110	115	120	
cat tct gat gaa tct gat gaa ctg gtc act gat ttt ccc acg gac ctg			1800
His Ser Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu			
125	130	135	140
cca gca acc gaa gtt ttc act cca gtt gtc ccc aca gta gac aca tat			1848
Pro Ala Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr			
	145	150	155
gat ggc cga ggt gat agt gtg gtt tat gga ctg agg tca aaa tct aag			1896
Asp Gly Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys			
	160	165	170
aag ttt cgc aga cct gac atc cag gtaaatectt taacagacac acctgatggt			1950
Lys Phe Arg Arg Pro Asp Ile Gln			
	175	180	
tctgactago gctcaagtct aggaaaccac agtttgcata ttcattcatt cattcatcca			2010
ttcattcato cattcagcaa gaattcattc atattctact ttatgaccat tgaatacaaaa			2070
tctttttctg cttggcggtt tttgtaagtc tacataatct ctctctagat ttgattctca			2130
aacacaatct tactttttga aatcctggat caaagtaaca tgctagtatt atttcagcca			2190
gatttagaca atttttagta taagatgacc taaaagctag agagtggaaa aggattacca			2250
tattcccatc cctagccgtt catataatta ttcttcattt gtgcgctgat tcag tac			2307
			Tyr
cct gat gct aca gac gag gac atc acc tca cac atg gaa agc gag gag			2355
Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser Glu Glu			
	185	190	195
ttg aat ggt gca tac aag gcc atc ccc gtt gcc cag gac ctg aac gcc			2403
Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu Asn Ala			
	200	205	210
cct tct gat tgg gac agc cgt ggg aag gac agt tat gaa acg agt cag			2451
Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Gln Thr Ser Gln			
	215	220	225
ctg gat gac cag agt gct gaa acc cac agc cac aag cag tcc aga tta			2499
Leu Asp Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser Arg Leu			
	235	240	245
tat aag cgg aaa gcc aat gat gag agc aat gag cat tcc gat gtg att			2547
Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp Val Ile			
	250	255	260

Phe His Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser Lys Glu
 280 285 290

gaa gat aaa cac ctg aaa ttt cgt att tct cat gaa tta gat agt gca 2691
 Glu Asp Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp Ser Ala
 295 300 305

tct tct gag gtc aat taa aaggagaaaa aatacaatctt ctcactttgc 2739
 Ser Ser Glu Val Asn
 310

atttagtcaa aagaaaaaat gctttatagc aaaatgaaag agaacatgaa atgcttcttt 2799

ctcagtttat tgggttgatg tgtatctatt tgagtctgga aataactaat gtgtttgata 2859

attagtttag tttgtggctt catggaaact ccctgtaaac aaaagcttca gggttatgtc 2919

tatgttcatt ctatagaaga aatgcaaact atcactgtat tttaatatctt gttattctct 2979

catgaataga aatttatgta gaagcaaaca aaatactttt acccacttaa aaagagaata 3039

taacatttta tgctactata atcttttgtt ttttaagtta gtgtatatatt tggtgtgatt 3099

atcttttgtg gtgtgaataa atcttttatc ttgaatgtaa taag 3143

<210> 24
 <211> 314
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)..(16)
 <223> Potential

<220>
 <221> Gene
 <222> (1)..(314)
 <223> Osteopontin

<220>
 <221> CHAIN
 <222> (17)..(314)
 <223> Osteopontin

<220>
 <221> SITE
 <222> (159)..(161)
 <223> Cell attachment site

<221> CARBOHYD
<222> (106)..(106)
<223> N-linked (GLCNAC...) (Potential)

<220>
<221> VARSPLIC
<222> (31)..(57)
<223> Missing (In Isoform C)

<220>
<221> VARSPLIC
<222> (58)..(71)
<223> Missing (In Isoform B)

<400> 24

Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
1 5 10 15

Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
20 25 30

Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
35 40 45

Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu
50 55 60

Glu Thr Asn Asp Phe Lys Gln Glu Thr Leu Pro Ser Lys Ser Asn Glu
65 70 75 80

Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His
85 90 95

Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp
100 105 110

Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu
115 120 125

Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu
130 135 140

Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg
 165 170 175

Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His
 180 185 190

Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala
 195 200 205

Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser
 210 215 220

Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His Ser His
 225 230 235 240

Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu
 245 250 255

His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu
 260 265 270

Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp
 275 280 285

Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His
 290 295 300

Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
 305 310

<210> 25

<211> 259

<212> PET

<213> Homo sapiens

<220>

<221> Gene

<222> (1)..(259)

<223> Carbonic Anhydrase domain of human carbonic anhydrase III

Glu Leu Phe Pro Asn Ala Lys Gly Glu Asn Gln Ser Pro Ile Glu Leu
20 25 30

His Thr Lys Asp Ile Arg His Asp Pro Ser Leu Gln Pro Trp Ser Val
35 40 45

Ser Tyr Asp Gly Gly Ser Ala Lys Thr Ile Leu Asn Asn Gly Lys Thr
50 55 60

Cys Arg Val Val Phe Asp Asp Thr Tyr Asp Arg Ser Met Leu Arg Gly
65 70 75 80

Gly Pro Leu Pro Gly Pro Tyr Arg Leu Arg Gln Phe His Leu His Trp
85 90 95

Gly Ser Ser Asp Asp His Gly Ser Glu His Thr Val Asp Gly Val Lys
100 105 110

Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Pro Lys Tyr Asn Thr
115 120 125

Phe Lys Glu Ala Leu Lys Gln Arg Asp Gly Ile Ala Val Ile Gly Ile
130 135 140

Phe Leu Lys Ile Gly His Glu Asn Gly Glu Phe Gln Ile Phe Leu Asp
145 150 155 160

Ala Leu Asp Lys Ile Lys Thr Lys Gly Lys Glu Ala Pro Phe Thr Lys
165 170 175

Phe Asp Pro Ser Cys Leu Phe Pro Ala Cys Arg Asp Tyr Trp Thr Tyr
180 185 190

Gln Gly Ser Phe Thr Thr Pro Pro Cys Glu Glu Cys Ile Val Trp Leu
195 200 205

Leu Leu Lys Glu Pro Met Thr Val Ser Ser Asp Gln Met Ala Lys Leu
210 215 220

Leu Asn Thr Asn Ile Thr Gln Pro Ile Asn Asn Arg Val Val Asn Ala

245

250

255

Ser Phe Lys

<210> 26

<211> 260

<212> PRT

<213> Homo sapiens

<220>

<221> Gene

<222> (1)..(260)

<223> Carbonic anhydrase domain of human carbonic anhydrase I

<400> 26

Ala Ser Pro Asp Trp Gly Tyr Asp Asp Lys Asn Gly Pro Glu Gln Trp
1 5 10 15

Ser Lys Leu Tyr Pro Ile Ala Asn Gly Asn Asn Gln Ser Pro Val Asp
20 25 30

Ile Lys Thr Ser Glu Thr Lys His Asp Thr Ser Leu Lys Pro Ile Ser
35 40 45

Val Ser Tyr Asn Pro Ala Thr Ala Lys Glu Ile Ile Asn Val Gly His
50 55 60

Ser Phe His Val Asn Phe Glu Asp Asn Asp Asn Arg Ser Val Leu Lys
65 70 75 80

Gly Gly Pro Phe Ser Asp Ser Tyr Arg Leu Phe Gln Phe His Phe His
85 90 95

Trp Gly Ser Thr Asn Glu His Gly Ser Glu His Thr Val Asp Gly Val
100 105 110

Lys Tyr Ser Ala Glu Leu His Val Ala His Trp Asn Ser Ala Lys Tyr
115 120 125

Gly Val Leu Met Lys Val Gly His Ala Asn His Lys Leu Val Lys Val

145 150 155 160

Leu Asp Ala Leu Gln Ala Ile Lys Thr Lys Gly Lys Arg Ala Pro Phe
165 170 175

Thr Asn Phe Asp Pro Ser Thr Leu Leu Pro Ser Ser Leu Asp Phe Trp
180 185 190

Thr Tyr Pro Gly Ser Leu Thr His Pro Pro Leu Tyr Glu Ser Val Thr
195 200 205

Trp Ile Ile Cys Lys Glu Ser Ile Ser Val Ser Ser Glu Gln Leu Ala
210 215 220

Gln Phe Arg Ser Leu Leu Ser Asn Val Glu Gly Asp Asn Ala Val Pro
225 230 235 240

Met Gln His Asn Asn Arg Pro Thr Gln Pro Leu Lys Gly Arg Thr Val
245 250 255

Arg Ala Ser Phe
260

<210> 27
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<221> Gene
<222> (1)..(337)
<223> Carbonic anhydrase domain of human carbonic anhydrase VIX

400 27

Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala Ala
1 5 10 15

Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln Asp His
20 25 30

Asp Ile Gln Thr Arg Ser Val Thr His Arg Ile Arg Leu Ile Ala Leu

50

55

60

Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu Pro Leu Asp Leu His
65 70 75 80

Asn Asn Gly His Thr Val Gln Leu Ser Leu Pro Ser Thr Leu Tyr Leu
85 90 95

Gly Gly Leu Pro Arg Lys Tyr Val Ala Ala Gln Leu His Leu His Trp
100 105 110

Gly Gln Lys Gly Ser Pro Gly Gly Ser Glu His Gln Ile Asn Ser Glu
115 120 125

Ala Thr Phe Ala Glu Leu His Ile Val His Tyr Asp Ser Asp Ser Tyr
130 135 140

Asp Ser Leu Ser Glu Ala Ala Glu Arg Pro Gln Gly Leu Ala Val Leu
145 150 155 160

Gly Ile Leu Ile Glu Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His
165 170 175

Ile Leu Ser His Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser
180 185 190

Val Pro Pro Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln
195 200 205

Tyr Phe Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser
210 215 220

Val Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln
225 230 235 240

Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro Ser
245 250 255

Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly Cys Leu Cys Leu
290 295 300

Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile Arg Lys Lys Arg Leu
305 310 315 320

Glu Asn Arg Lys Ser Val Val Phe Thr Ser Ala Gln Ala Thr Thr Glu
325 330 335

Ala

<210> 28
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 28
cagcagttgg atggaagagg ac 22

<210> 29
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 29
cactgagatt ctggcactat tc 22

<210> 30
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<210> 31
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 31
ttgactggct caggagtata g 21

<210> 32
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 32
ctgataatga gggctcccaa c 21

<210> 33
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 33
ctctgcactt cctggtaaaa ctct 24

<210> 34
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 34
cagcagttgg atggaagagg ac 22

<220>

<223> Primer

<400> 35

ctctgcactt cctggtaaaa ctct

24